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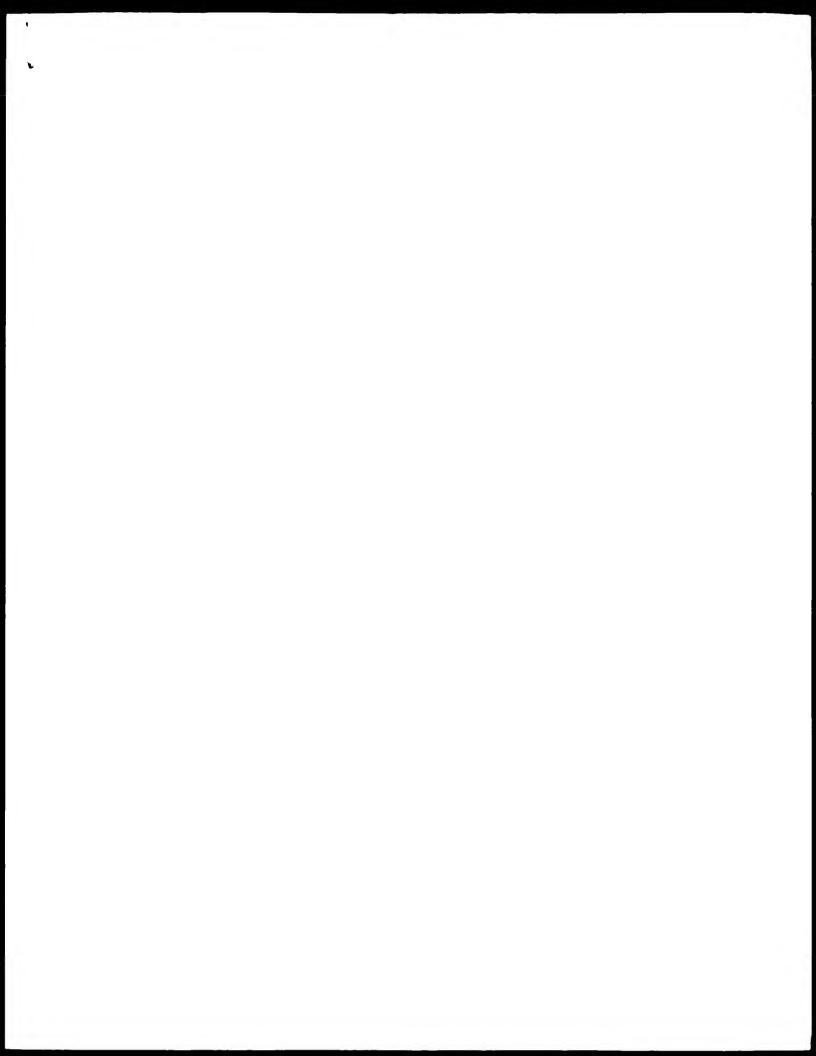
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DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Appert,C., Logemann,E., Hahlbrock,K., Schmid,J. and Amrhein,N. Structural and catalytic properties of the four phenylalanine ammonia-lyase isoenzymes from parsley (Petroselinum crispum Nym.) Bur. J. Blochem. 225 (1), 491-499 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids II; Apiales; Apiaceae; Petroselinum.

[ (bases 1 to 2403)]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (22-AUG-1994) C. Appert, Institut fuer pflanzenwissenschaften, Eidgenoessische Technische Hochschule, zuerich, Universitaetsstrasse 2, 8092 Zurich, SWITZERLAND Location/Qualifiers
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AAOKLHEMDPLOKPKODRYALETSPOMLGPOLEVI RSSTKMI EREI INSVINDHPLIDVS
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ILKLMSTTFLVGLCQAIDLIHLEENLKSTVKNTVSQVAKRVLTMGVNGELHDSRFCEK
DLLRVVDREYIFAY IDDPCSATYPLMOKLRETUVEHALNINGDKERILSTSIFOKI AAF
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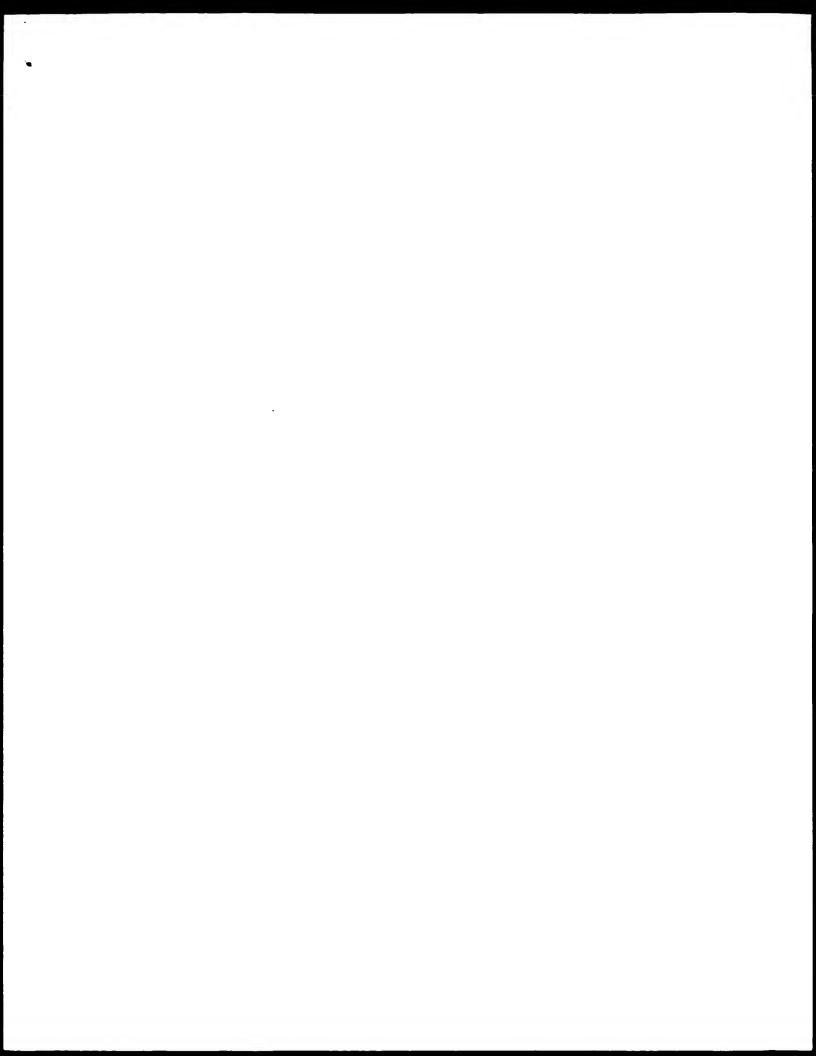
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Query Match 52.0%; Score 1270.8; DB 8; Length 2403: Best Local Similarity 74.2%; Pred. No. 1.1e-293; Matches 1634; Conservative 0; Mismatches 562; Indels 6; Gaps

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1202	MINIGETETTAGAACATETECTCAATGGCTTGGTCCTCAAATTGAAGTTATCAGATCAT		45
N N	TATGCTCTCCGTACATCTCCCCAATGGCTCGGACCTCAAATCGAAGTAATCCGATCAT		δ
1142	GTTAAGGCTGCTCAAAAGCTACATGAAATGGATCCATTACAAAAACCAAAACAAGACA	1083	Db
1151	CAAGGCGGCGAAAAGGTCCACGAAATGGACCCGTTACAGAAAACAAAACAAGATC	1092	Qy
1091	ALCACCCISSICAAATCSAGSCGSCGSGCATCATGGAGTATATTTTGGACGGAAGCGATT	1023	B 4
02	GCTGAAGTGATGCAAGGGAAGCCTGAATTTACCGACCATTTGACACATAAGTTGAAGC	96	D D
1031	ATGCAAGGGAAGCCGGAGTTTACCGATCACTTGACACACAAATTGAAGC	972	Qy
σ.	TATGGTACTTTTGAGGCTAATATATTAGCAGTTTTAGCTGAAGTTATGTCAGCAATTT	903	DЬ
7	VIGCTAATGTACTTGCGTTGTTGTCGGAAGTGTTATCGGCGATCT	912	VΩ
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842	TAACACTCAGCCCCGAAGAAGCATTTAAGCTTGCTGGTGTGGAAGGTGGATTTTTTGAGT	783	Дb
851	CCTCAATGCCGAAAAAGGCCTTCGCTGCAGCCGGAGTTGAAGGTGGGTTCTTCGAGT	792	Qy
782	ATTGCTGGACTTCTCACTGGTCGTCCCAACTCCAAGGCTGTTGGACCGACTGGAG	N (B 5
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662	CTATTCAGGAATCCGATTCGAGATCCTTGAAGCCATCACCAAGTTTCTTAACCACAACA	603	Дb
671	TACTCCGGCATCCGATTCGAGATCTTGGAAGCCATCACCAAGTTCCTTAACAACAACA	612	Qy
611 602	CACTTCCACATTCAGCCACCAGAGCCGCCATGATCGTCAGAATCAACACCCTCCTCCAGG	552 543	Дb
542		483	Вb
551	STCATTAGATTTTTGAACGCCGGAATATTCGGCAATGGAACGGAAACAAGC	495	Qy
494	CTACTGGCTTTGGTGCTACTCTCATAGGAGGACTAAACAAGGTGGTGCTTTACAAAAGG	423	pb 45
N	GCTAGTAGTGACTGGGTGATGGATAGTATAAAGGGACGGATAGTTATGGTGTTA	on on	Db C
434	ATGAATAAAGGAACTGATAGTTATGGTGTCA	375	Qy
on .		306	Db
~J	ACACCGTGAAGGTGGAGCTGTCGGAAGCCGCGAGGGCTGGAGTTA	315	Qy
31 4 305	AGCCGGTGGTGAAGCTCGGAAGAAGAAGACGCTTACAGTTTCTCAGGTGGGGGATCGCAAGACGCTTACAGTTTCTCAGGTGGCGGGATCGCAAGTTTTCGGAAGCTGCTAATTTCGGAAGCTGGCTAATTTCGG	255	Db Qy
245	SAGGCATTGACAGGGAGTCAT	186	DЬ
254	GGAGGCGTTGACCGGAAGTCACCTTGATGAGGTGAAGAAGATGGTTGCGGAGTTC	195	Qy
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SUMMARIES

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ALIGNMENTS

REFERENCE	AF299330 LOCUS DEFINITION ACCESSION VERSION VERSION KEYWORDS SOURCE ORGANISM	RESULT 1
EMATYOGA; VITIGIP:antac; Streptophyta; Embryophyta; Trachophyta; Spermatophyta; Magnoliophyta; endirotyledons; core endirots; Asteridae, enasterids II, Asterales, Asteracee, Lactuceae; Lactucea. 1 (bases 1 to 2442) Campos-Vargas,R., Nonogaki,H., Suslow,T. and Saltveit,M.	AP299330 2442 bp mkNA linear PLN 31-DEC-2001 Lactude sativa phenylalanine ammonia-lyase mkNA, complete cds. AF299330 AF299330.1 GI:18001006 Lactude sativa.	

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                                                                                                           TAGTTATGGTGTCACCACCGGCTTCGGCGCCACCTCTCACCGGAGAACTAAGCAAGGCGG 480
                                            TGCTTTACAGAAGGAGCTCATTAGATTTTTGAACGCCGGAATATTCGGCAATGGAACGGA 540
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REYVFAYIDDVCSGTYPLMQKLRQVLVDHALNNGETEKNTNTSIFQKIATFEEELKVL
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MDPLQKPKQDKYALRTSPQWLGPQIEVIKSSTKMIEKEINSVNDNPLIDVSRNKALHG
GNEQGTPIGVSMDNTRLAIAAIGKLMEAQESELVNDFYNNGLPSNLSGGRNPSLDYGF
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YGVTTGFGATSHRRTKQGGALQKELIRFLNAGIFGNGTETSHTLPHSATRAAMIVRIN
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/protein_id-"AAL55242.1"
/db_xref-"GI:18001007"
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AAAGGTGGAGAAATCGCCATGGCTTCTTACTG 15	1 ACGTAACCGTAGTTTGGACTACGGGTTCAA	1441	Оу
		1441	
AACAATGGATTACCATCGAATCTCTCCGGTGG 1	1 AFTTTCIGAGCTGGTTAACGATITCTACAA(1381	Qy
		1381	Db
ATTGCTGCAATCGGAAAACTCATGTTCGCTCA 13	AGTITCCATGGACAACACCGTCTCGCCAT	1321	Qy
		1321	db
TACACGGTGGTAACTTCCAAGGAACCCCAATCGG 1320	GATCGACGTTTCCAGAAACAAAGCTTTA	1261	Qy
		1261	dd
BAGAGGAAATCAATTCCGTCAACGACAACCCATT 1260	AATCCGATCATCAACCAAAATGATCGAGAC	1201	dq
		1201	qq
POTOCOCAATGACTCGGACTCAAATCGAAGT 12	AAAACAAGATGSTTATGSTTCCSSTACATG	1141	Db
		1141	Qy
rccacgaaarggacccgr - - - - - - - - - - - - - - - - - - -	. CGGAAGCGATTACGTCAAGGCGGCGCAA	1081	ДУ
DGGCGGCGATCATGGAGTATATT	CAAATTGAAGCATCACCCTGGTCAAATCGAC	1021	da
		1021	VQ
AAGGGAAGCCGAGTTGACA	ATCGGCGATCTTCGCTGAGGTTATGCAAGC	961	qa
		961	Ao
ATGCIAAIGTACITGCGTTGTTGTCGGAAGTGTI 960 	TGC	901 901	ФФ
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GGCTTCGCTGCAGCCGGACTTGAAG	CCCCACCGGAGAAGTCCTCAATGCCC	781	Dp
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podelogolosaaceambaceolosicooloacei 720	1 TAACAACAACAPCACCCCTIGTTTACCCCIC	661	dd
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SATTOGAGATOTTGGAAGCCATCACCAAGTTCCT 660 	CGGCATCCGAT CGGCATCCGAT	601 601	Qy Dh
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Local Similarity 81.1%;
                                                                                381 GTAGTGATTGGGTTATGGAGAGGATGAATAAAGGAACTGATAGTTATGGTGTCACCACCG 440
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (11-FER-1998) F.A. Maregrat, "A INFA / "VIV, Indirencite Blaise Pascel, Campus des Cezeaux, 63177 Aubiere cedex, FRANCE on Feb 14, 1998 this sequence version replaced girl934868.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Evidence for multiple copies of formate dehydrogenase genes in plants: isolation of three potato fdh genes, fdhi, fdh2, and fdh3 (Arcession Nos 249442, Z34443 and AlEn4829, respectively). (PGR98-102)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (09-APF-1997) F.A. Mazeyrat, HA INFA / OVGV, Universite Blaise Pascel, Campus des Cezeaux, 63177 Aubiere cedex, FRANCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        plant Physicl 117,
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/protein_id="CAA/3065.1"
/protein_id="CAA/3065.1"
/db_xref="G1:2887304"
/db_xref="S01:28-PROTE004058"
/translation="MENGTHYNGSANGFCIKDPLNWGVAAFALTGSHIDFYKKMYGEF
/KRYVKLFGETLTYSLYAGISAAGDENNYKVELSEAARAGVKASSDWYMESMNKKTDS
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GNEGGTPIGVSMDNTRLAIAALGKVTIAGEVSELVENETYNNGLSILLSGGRNPSLDSGF
KGGEELMASYSCSELGELANEVY INVUSAEUHNGLOVENSKILLSGGRNPSLDSGF
TYLVALTGS INJEHILEENMYSTVKITVSGAVKVILTMGVVTSEHIFSPITGEKULLKVVI
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                                                      ACGGGTTCAAAGGTGGAGAAATCGCCATGGCTTCTTACTGTTCTGAGCTTCAGTTTCTCG
                                                                                                                                               ATTTCTACAACAATGATTACCATCGAATCTCTCCGGTGGACGTAACCCTAGTTTGGACT
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                                                                                                                  ATTTTTATAACAATGGGTTGCCTTCGCATTTGTCGGGTGGGCGTAACCCAAGTTTGGATT
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                                               Rehmannia glutinosa.
Rehmannia glutinosa
Rehmannia glutinosa
Eukaryota; Viridiglantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiglantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Lamiales; Lamiales incertae sedis;
  Yun,S.J.,
                                                                                                                                                                                            complete cds. AF401636
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                                                                                                                                                                                                                                 Rehmannia glutinosa phenylalanine ammonia-lyase (PAL1) mRNA
                                                                                                                                                                                                                                                          AF401636
                                         Rehmannia.
                  (bases 1 to 2444)
Lee, B.K.,
                                                                                                                                                                            GI:15100058
  Park, M.R.,
                                                                                                                                                                                                                                                      2444 bp
  Srinivas, B.
                                                                                                                                                                                                                                                        mRNA
and Chun, J.-C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    114 TAATAATGGAGAACGGTAATGACGTTAATGGAGTCGTTAATGAGTTGTGCATCAAGGATC 173
                                                                                                                                                                                                                                                                                                       GAACTGATAGTTATGGTGTCACCACCGGCTTCGGCGCCCACCTCTCACCGGAGAACTAAGC 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTCAGGTGGCGGGGAGCTGCTAATGACAGTGACACCGTGAAGGTGGAGCTGTCGG 353
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AAGGTGGTTGCTTCAGAAGGAGCTCATTAGGTTCTTGAATGCCGGAATATTCGGCAACG 522
                                                                                                                                                                   AAGGCGATGATTTATAGAAGAATTTATTAGATTTTTGAACGCCGGAATATTCGGCAATG 533
                                                                                                                                                                                                                                       GGACTGACAGTTATGGAGTTACAACGGGTTTTGGGTGCCACGTCACATAGGAGGACTAAAC 462
                                                                                                                                                                                                                                                                                                                                                                      AGACUSCGCGTGCGSAGGGTAAGGCAGGTAGCGATTGGGTTATGGAGAGTATGAATAAAG 402
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Submitted (23-JHI-2001) Faculty of Biological Resources Sciences
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52.7%; Score 1286.2; DB 8; Length 2444,
Similarity 72.6%, Pred. No. 2.20-297;
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EIAMASYCSELQFLANPVTNHVQSAEQHNQDVNSLGLISSRKTVEALDILKLMSSTYL
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VTSV FFAEVNNGKPEFTDHLTHKLKHHPGQLEAAATMEHTLDGSAYVKAAQKLHETDP
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RKPAVKLGGESLTIAQVAAIAARDNAVAVELAETARAGVKASSDWYMESHNKGTDSYG
VTTCFGATSHRATKGGALQKELIRFLNAGIFGNGTESHNALPHSATRAAMLVRAUTL
LOGYSGIRFEILFALTKFLNHNITPCLPLRGTITASGDLVPLSYIAGILTGRPNSKAV
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/protein_id="AAK84225.1"
/db_xref="G1:15100059"
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/EC_number-"4.3.1.5"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CGAAGAGGACTCTGACAATGGGTATTAATGGCGAACTTCATCCGTCAAGATTCTGCGAGA 1779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGAAAAAGGTCCTCACCATGGGCGTCAACGGCGAGCTCCACCCGTCGAGATTCTGCGAGA 1793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTTGAGGCACTTGGAGGAGAATTTGAGGCTTTCAGTTAAAAACACCGTTAGCCAAGTGG
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                                                                                                                                                                                 pal4 gene.

Petroselinum crispum.

Petroselinum crispum.

Petroselinum crispum.

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                       Schulz,W., Eiben,H.G. and Hahlbrock,K.
Expression in Escherichia coli of catalytically active phenylalanine ammonia-1yase from parsley
FEBS Lett. 258 (2), 335-338 (1989)
                                                                                                                                 Asteridae; euasterids II; Apiales; Apiaceae; Petroselinum 1 (bases 1 to 2375)
                                                                                                                                                                                                                                                                                                                              P.crispum RNA for PAL4, phenylalanine ammonia-lyase
                                                                                                                                                                                                                                                                                                                                                          PCPAL4
2689222
                       90092501
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                     1067 GAGTATATTTTGGACGGAAGCGATTACGTCAAGGCGGCGCAAAAGGTCCACGAAATGGAC 1126
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                                                                   969 GACCACTTGACACATAAGTTGAAGCATCATCCAGGACAAATTGAAGCAGCTGCTATAATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              609 ATTACAAAGITTCTCAACCAAAAATTACTCCTTGCTTGCCACTCCGTGGAAAGATCACT
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                                                                                                                                                                                                                                                                                                                                               GATCACTTGACACAAATTGAAGCATCACCCTGGTCAAATCGAGGCGGCGGCGATCATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCCTCCGGTGACCTTGTCCCATTATCATACATCGCCGGCCTCTTAACCGGCCGCCCCAAC
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                                                                                                                                                                 TTAGCTGAGGTTATGTCGGCTATATTTGCTGAAGTGATGCAGGGCAAACCTGAATTTACT 968
                                                                                                                                                                                                                                                                                   ACCCCCTGGGGTCCGGGATGGCTTCCATGCTTCTATTTGATGCTAATGTACTTCCGTTG 946
                                                                                                                                                                                                                                                                                                                                                                                             GGAGTTGAAGGTGGGTTCTTCCAGTTACAGCCCAAAGAAGGGCCTAGCACTTGTTAACGGC 886
                                                                                                                                                                                                                                                                                                                                                                                                                                           TCCAAGGCGGTTGGACCCACTGGAGAAAACCTGACCGCTGCAGAAGCATTTAAACTTGCT
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Pred No 4 8e-296;
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                        GGAGAGGACTTCCAACAGGGTGTTCAA-SSS-CATCITSCAAAASITCAAAATATTCAATCCGTTG 2266
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTTT97A90;93:A:ATA632A1TAAT9:A3AA32CD20;4A:33TTCT343PC3ACCACGCT_1906
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GGAGAGGAGTITTCACAGCTIGTTTTACAGCAATGTGGAAAGGTCAGTCATTCATTCTTTTG
                                                                                                                                                                                                                                                        GAGAATGATACATTGTGGATTGTCAAACAGATAAAGCTTGCAGATGGTACCGTTGTAT 2086
                                                                                                                                                                                                                                                                                                                                         TTTGAAGAAGTTGAAGGCTCTCTTGCCAAAGGAGGTTGAAAGTGCAAGGGCTGTGCTA 1988
                                                                                                                                                                                                                                                                                                                                                                                                TTCGAAGAAGAATTGAAAGTGGTGTTATEGAAAGTTGAAGGTGTTAGAATCGCTTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTGAAAAATGGCGAAAACTGAGAAAGAATTTGAGCACCTCAATCTTCCAAAAGATTGCAGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Appert,C., Logemann,E., Hahlbrock,K., Schmid,J. and Amrhein,N. Structural and catalytic properties of the four phenylalanine ammonia-lyase isoenzymes from parsicy (Petrosclinum crispum Ny Eur. J. Blochem. 225 (1), 491-499 (1994)
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Petroselinum crispum
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1 (bases 1 to 2403)
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AMLVRINTLIAGYSGIFEELLEAITKEINHNITPCLEFRGTITASGLUVPLSYIAGLL
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EAN LAVLAEVMSA FFAEVMOGKPEFTDHLTHKLKHHPGQI EAAA I MEH I LIXGSAYVK
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FSLIVGFKGAEIAMASYCSELUFLANFYT NIPUSAEUHNULVNSLGLI SSKKTSEAVE
                                                ILK LMSTTPLVGLCQATDLPHLEENLKSTVKNTVSQVAKRVLI MSVNGELHDSRPCEK
DLLPVVDPRY I FAY I DDPCSATY PLMQKLPETLVEHALNNGDKERNLSTS I FQK I AAF
EDELKALLPKEVETARAALESGNPA I PNR I KECRSYPLYKFVREELGTEYLTGEKVRS
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89. .2245
                             PGHEFEKVFTAMSKGETIDPLLECLESWNGAPLPIC"
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/translation="mayvnGTTnGHanGnGlDlCmkKEDPLnwGvaaFalIGShIDEV
KRMVAEYKKPVVKLEGETLTISQVAAISARDDSGVKVELSEEARAGVKASSDWVMDSM
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/db_xref="GI:535008"
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Submitted (06-DEC-2000) Division of Biochemistry, Bioresources Submitted (National Institute of Agricultural Sciences and Department, National Institute of Agricultural Sciences and Council Counci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 (bases 1 to 2448) 
 Kim,J.-B., Kim,J.-B., Cho,K.-J., Woon,U. and Ha,S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kim,J.-B., Kim,J.-B., Cho,K.-J., Woon,U. and Ha,S.-H. Molecular Cloning and Characterization of Phenylalanine Ammonia-lyase(PAL) Related to the Biosynthesis of Rosmarinic in Agastache rugosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta, eudicotyledous, core eudicots;
Asteridae; euasterids I; Lamiales; Lamiaceae; Agastache.
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                                                                                                                                                                                            GGAACCCCCATTGGAGTATCCATCGACAACACCAGATTAGCCATTGCCTCCATCGGGAAG 1353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCTCAGATICGAAGTCATICGGCACCCCACCAAGATCALCGAGCGGGAGATCAACTCCGTIC 1237
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                                                   AUTHORS
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                 Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.

1 (bases I to 2462)
Pellegrini, L., Rohfritsch, O., Fritig, B. and Legrand, M.
Phenylalanine ammunia-lyase in tubaccu. Mojecular cluning and gene
expression during the hypersensitive reaction to tobacco mosaic
                                                                                                                                                                      Nicotiana tabacum
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                               438 CCGGCTTCGGCGCCACCTCTCACCGGAGAACTAAGCAAGGCGGTGCTTTACAGAAAGGAGC
                                                                                                                                                                                                                       324 AAGATAATGCTAAAACTGTAAAAGTGGAGCTTTCTGAAGGAGCAAGAGCTGGTGTTAAAG
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                                                                                                          384 CTAGTAGTGATTGGGTTATGGATAGTATGAGTAAAGGAACTGATAGTTATGGTGTTACTA
                                                                                                                                                                                                                                                                             318 CTAATGACAGTGACACCGTGAAGGTGGAAGCTGTCGGAAGCCGCGAGGGCTGGAGTTAAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81 TTTCTTTGATCTATAGTCTACAATCTGTATAAATAATAATGGAGAACGGTAATCACGTTA 140
                                                                                                                                            CGAGTAGTGATTGGGTTTATGGAGAGGATGAATAAAGGAACTGATACTTATTGGTGTCACCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             virus and the response to a fungal elicitor plant Physiol. 106 (3), 877-886 (1994) 95125127
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VFSEVLSAIFAEVMNCKPEFTDHLTHKLKHHPGOIEAAINEHILDGSSYVKAPOKLH
ETDPLQKPKQDRYALRTSPQWLGPIEVIRASTKMIEREINSVNDNPLIDVSRNKALH
GRNEGGTPIGVSMDNARLALASIGKLHFAQFSELVNDYNNGLPSNLTAGRNESLDYG
FKGSEIAMASYCSELQFLANPVTNHVQSAEQHNQDVNSLGLISARKTAEAVDILKLMS
STYLVALCQAIDLRHLEENLRNAVKNTVSQVAKRTLTMGANGELHPSRFCEKDLLRVV
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4 488 c 547 g 680 t
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SYGVTTGFGATSHRRTKNGGALQKELIRFLNAGVFGNGTESCHTLPQSGTRAAMLVRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="phenylalanine ammonia-lyase"
/protein_id="CAA55075.1"
/db_xref="GI:633597"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 72 hrs after infection by Tobacco Mosaic Virus (TMV)" (dev_stage="30 day old"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VLPKEYESARISLENGNPAIANRIKECRSYPLYRFYREELGAELLTGEKVRSPGEECD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="SWISS-PROT:P45733"
/translation="MAGVAQNGHQEMDFCVKVDPLNWEMAADSLKGSHLDEVKKMVAE
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/clone_lib="Lambda ZAP II vector, cDNA from tobacco leaves
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=:
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71.8%;

    Mismatches

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1518 TOGGAAATOCAGTGAGGAGGAGGATGAAAGGGGGGGAAGAAGAAGAAGAGGGTTAATT HILLIHHH HILHIH HILHIHHHHHHHHHHHHH	ОУ
1458 ACTACGGGTTCAAAGGTGGAGAAATCGCCATGGCTTCTTACTGTTCTGAGCTTCAG 	£ 64
1398 ACMATTECTANAMATAGATTACOATSAATCTCTSAGGAGGAAGGAATCAAGCAAGCAAGCAACAACAACAACGATTGCCATCTAATCTGACAGCAGCAAGGAATGCAAGC	94 65
338 CCCGTC 344 CTAGAI	Db Oy
78 ACAAAGCT	Db Qy
18 AAATGATCGAGAGAGGAAATCAATT	Qу
58 CHCHCCGTA 64 CHTTAGAA	DЪ
1098 AGGCGGGGCAAAAGGTCCANGAAATGGANNOGTTACAGAAAANAANAAAAAAACGTT 	рь Оу
88 CIGGICAAA 44 CCGGACAAA	90 45
78 84	ОУ
18 TICIATITGATGCIAATGTACTF3.GT 	Dp GA
858 CGAAAGAARAGACACTTAGTTAACGACACACTTAGGAGAGAGAGAGAGA	qa Að
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38 44	م م
678 CITGITTACCECCTECGIGGAACCATCACCGCTCCGGIGACCTTGICCCATTATCATACA	Db
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558 CACATTOM-SOLOCAGAGO CACAGATOATOATACAAATACACTOCTOCTOCAGGTT 	dd Gy
98 TCATTAC 04 TAATTAC	9 10 4 0 4

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                                                                                                                                                                                                                                                                                                                                                                                                                                                              TATTGACAGGAGAAAAGTCAGGTCAGGTGAAGAAGTGTGACAAAGTGTTGACAGGAA
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AAATGAAAAGTGACAA 2435
                                           AAAAAAAAAAAAAA 2433
                                                                                     GTAAACTCTGTTGAATATGTTGGT ---TIGTAGTTATATAAGICTCTTTTCAGTAAAAAT 2419
                                                                                                                                                                                                                              GTTTTTTTTTTTTTTTAAATTTTATTTGCATTTAATATCTCATCAAAACTTCCACT
                                                                                                                                                                                                                                                                          CTCTTCCAATCTCTTA-GAAGTTGGTTCTCAAACAACACACCTTTGTTTATGTTTGTCA 2302
                                                                                                                                                                                                                                                                                                                   CTCTTCCAATATGTTAGGAAAGTGAGTGTGAAAGCGTTTGAATTGTATTTGTAATATTCT 2297
                                                                                                                                                                                                                                                                                                                                                                                             | TGTGCAAAGTCAAATTATTGATCCGTTGGTTGGAGGTTGGCATGGGAGGGGGAATGGGGGAAC
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                                                                                                                                 TTCAACTGTGCTCTTATGTGGTTGTAAATCATATATTATTAACTTATTATTTTTGGTAAAAA 2417
                                                                                                                                                                               ATTACTTCTTATTTTCTATTAATTTTATATTTACTTTTCTTTTTCAGCTTCATTAATT 2362
                                                                                                                                                                                                                                                                                                                                                                       TGTGCAATGGACAAATTATTGATTCATTAGTAGAGTGTCTCAAGGAA1GGAATGGTGCTC
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RESULT 8

ACCESSION VERSION SOURCE KEYWORDS DEFINITION

CMEPAL 2330 bp mRNA linear PLN 06-FE Camellia sinensis mRNA for phenylalanine ammonia-lyase (PAL), complete cds. PLN 06-FEB-1999

D26596 1 GI.662270

ORGANISM clone_lib:lambda gtll clone:A21.
Camellia sinensis phenylalanine ammonia-lyase; PAL. Camellia sinensis (cultivar:Yabukita) young leaf cDNA to mKNA,

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

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TITLE
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480 CATAGGAGGACCAAAGAAGGTGGTGCTCTTCAAAAGGAGCTTATTAGGTTCTTGAATGCT 539
                                                                                                                                                                                                                                                                                                              246 TTGGAGGAAGTGAAGGGCATGGTGGAGGAGGTTTCGGAAGCCAGTGGTGAGGCTGGGAGGG
                                                                                                                                                                                                                                                                         278 GAGACGCTTACAGTTTCTCAGGTGGCGGGGATCGCAGCTGCTAATGACAGTGACACCGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
                                    CACCGGAGAACTAAGCAAGGGGGTGCTTTACAGAAGGAGCTCATTAGATTTTTGAACGCC 517
                                                                                                GAGAGCATGAATAAAGGAACTGATAGTTATGGTGTCACCACCGGCTTCGGCGCCACCTCT
                                                                                                                                                       GCGGTGGAGCTGTCGGAGTCTGCGAGGGAGGGAGGGAGTGAAGGCCAGTAGTGATTGGGTTATG
                                                                                                                                                                                              AAGGTGGAGCTGTCGGAAGCCGCGAGGGCTTGAAGTGAGTTAAGGCGAGTAGTGATTTGGGTTATG 397
                                                                                                                                                                                                                                                                                                                                                     CTTGATGAGGTGAAGAAGATGGTTGCGGAGTTCAGAAAGCCGGTGGTGAAGCTCGGAGGA 277
                                                                                                                                                                                                                                                                                                                                                                                            GAGAGTATGAATAAAGGGACAGATAGTTATGGTGTTACTACTGGTTTTTGGTGCTACTTCA
                                                                                                                                                                                                                                     GAGACTTTGACGATATCGCAGGTGGCGGCGATCGCGG-----TGAGGGGGTAGTGAGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matsumoto, S., Takeuchi, A., Hayatsu, M. and Kondo, S. Molecular cloning of phenylalanine ammonia-lyase cDNA and classification of varieties and cultivars of tea plants (Camellia sinensis) using the tea PAL cDNA probe Theor. Appl. Genet. 89, 671-675 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Spermatophyta; Magnoliophyta; eudicotyledons, core eudicots.
Asteridae; Ericales; Theaceae; Camellia.
1 (Sites)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (22-JAN-1994) Satoru Matsumoto, Nati. Res. Inst. Vegetables, Ornamental Plants and Tea; Kanaya 2769, Kanaya, Shizuoka 428, Japan (Tel:0547-45-4101, Fax:0547-46-2169)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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2330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="MOSTTAJGNGVOSGGSPGFCLKDPLNWGVAAEAMKGSHLEEVKG
MVEEFRKPVVRLGGETLTISQVAAIAVRGSEVAVELSESAGVKASSDWYMESMNKG
TDSYGVTTGFGATSHRATKEGGALQKELIRFLNAGIFGNGTESCHTLPGSATRAAMLY
RINTLLQGYSGIRFEILEAISKFLNNNITPCLPLRGTITASGDLVPLSYIAGLLTGRH
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MSSTYLVALCQAYDLRHFEENLRNTYKSTYSQYAKRYLTMGYNGELHPSRFCEKDLLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LAVLSEVLSA I FAEVMOGK PEFTDHLT HKLKHHPGQ I EAAA I MEH I LDGSSYVKAAQK
LHEMDPLOKPKODRYALRTSPOMLGPL I EV I RSSTKS I ERE I NSVNDNPL I NVSRNKA
LHGGNFQGTP I GVSMDNTRLAVAS I GKLMFAQFSELVNDFYNNGLPSNLSGGRNPSLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="phenylalanine ammonia-lyase"
/protein_id="BAA05643.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref-"taxon:4442"
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                                                                                               CATGTCCAAAGCGCCGAGCAACATAACCAAGATGTGAACTCTTTAGGCCTAATCTCTTCA 1619
                                                                                                                                                                                               CATGTTCAAAGCGCCGAACAACAATCAAGACGTTAATTCTCTCGGATTAATTTCAGCG 1597
                                                                                                                                                                                                                                                                                               GAGATTGCCATGGCTGATTGCTCAGAACTCCAATTCCTTGCCAATCCTGTAACCAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGTGAGTGTGAAACCGTTTGAATTGTATT 2286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACGGTGAGCCAAGTAGCGAAGCGCGTTCTAACTATGGGCGTTAACGGAGAGCTTCACCCT 1799
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           Submitted (25-AUC-1993) Mitsuo Okazaki, Faculty of Textile Science and Technology, Shinshu Univ., Department of Applied Biology; 3-15-1 Tokida, Ueda, Nagano 386, Japan (Tel.0286-22-1215(ex.255).
                                                                                                                                                                     Cloning and sequencing of a full-length cDNA coding for phenylalanine ammonia lyase from tobacco cell culture plant physicl. 104 (3), 1091-1092 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                          D17467
D17467.1 GI:2570155
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                                                                                                                                                                                                                                                                                  Asteridae; euasterids I, Solanales; Solanaceae; Nicotiana
                                                                                                                                                                                                                                                                                                             Bukaryota; Viridiplantae, Streptophyta, Embryophyta; Tracheophyta
Spermatophyta, Magnoliophyta; eudicotyledons; core eudicots;
                                                                                                                                                                                                                                                                                                                                                                               Nicotiana tabacum cell line Bright Yellow T-13 cDNA to mpNA
                                                                                                                                                                                                                                                                                                                                                                                                       phenylalanine ammonia-lyase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOBPALL 2527 bp mRNA linear PLN 04 TOBACCO mRNA for phenylalanine ammonia lyase, complete cds
Fax:0268-22-4079)
                                                                                     Direct Submission
                                                                                                               ∩kazaki,M
                                                                                                                                                                                                                                                                                                                                                          Nicotiana tabacum
                                                                                                                                                                                                                                                                    (sites)
                                                                                                                                  (bases 1 to 2527)
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           SR2 SGAACTTATTAGGTTCTTGAATGCTGGAGTTTTTGGCAALGGAACAGAGTCATGGCAACAC
                                                                                                   462 TAAAGCTAGCAGTGATTGGGTTATGGACAGTATGGGTAAAGGAACTGATAGTTATGGTGT 521
                                                                                                                                                                                                                                                                                     402 TGCAAAAGATAATGTTAAAACTGTTAAAGTGGAGCTTTCTGAAGGGGGCAAGAGCTGGTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          193 AGCGGAGGCGTTGACCGGGAAGTCACCTTGATGAGGTGAAGAAGAAGATGGTTGGGGGAGAGTTCAG 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          222 AAATGGTCACCAAGAAATGGATTTTTGCATGAAAGTGGATCCATTAAACTGGAATGGC
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                                                                                                                                                                                                                                        RTR TAAGGGGAGTAGFGATIGGGTTATGGAGAGAGTATGAATAAAGGAAACIGATAGTTATGGTGT
                                                                                                                                                                                                                                                                                                                                                                                                                       AGCTGCTAATGACAGTGACAGCGTGAAGGTGGAGGTGTGGAGCTGCAAGCCGGCGAGGCTGGAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      741
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2527
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VPSEVLISA I FABYMNOKPEETDHLTHKLIKHHPGO I FAAA I MEH I LIDGSSYVKAAGKLH
ETDHLGVEKODEN ALERTSPOMLOED I TEXATIKMI E EETINSVUNDI LIDVSRIKKALII
GGNEGOT PIGVSMDARLALAAS I SKLMFQOFESLVNLY YNNSLESNLTAGRINESLDYG
EKGSEIAMAS YCSELQFLANPVINIIVOSAEGIINODVNSLDLI SARKTALADVDLIKLMS
STYLVALCOALDLRHLENLRNAVKNITVSOVAKKTLING I NGELHPSHECEKDLLKVV
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KVFTAMCNGGTIDSLLECLKEWNGAPLPTC"
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/db_xref="GI:2570156"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MAGVAQNGHQEMDFCMKVDPLNWEMAADSLKGSHLDEVKKMVAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="phenylalanine ammonia-lyase"
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71.8%; Pred. No. 6.9e-289;
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1633 CATGTCGTCGACATACTTAGTCGCTCTATGCCAATCCATCGATTTACGCCATTTGGAAGA 1692
                                                                                                    1662 GAACTCCTTGGACTTAATCTCAGCTAGAAAAAAAACAGCTGAAGCCGTGGACATCTTAAAGCT 1721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1453 TTTGGACTACGGGTTCAAAGGTGGAGAAATCGCCATGGCTTCTTACTGTTCTGAGCTTCA 1512
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AACCAAGATGATTGAGAGGGAGATTAATTCAGTGAACGACAACCCTTTGATCGATGTTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2381 TGTCAATTACCTGTTATTTTCTATTTTTACTTTTTCTTTTTCGGGGTTGATTAAATGTAA 2440
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                                                                                                                                                                                                                                                                                            Catharanthus roseus
Direct Submission
                           Kiyota, S
                                                                                                   cDNA of phenylalanine
                                                                                                                                    Kiyota, S
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                                                                                                 GTTCCTTAACAACAACATCACCCCTTGTTTACCCCTGCGTGGAAACCATCACCGCTCCGG 714
                                                                                                                                                                                                                      CAACAGGCTTCCTTCCAGGGTTTACTTCCGGCATTCCGATTTCGAGATCTTTGGAAGCCATCACCAA 654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGATGCTAGGGTTGGTTAAAGCCAGAAGAAGATTGGGTGATGGAGAGAAGCATGAATAAAGG 454
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AATAATGGAGAACGGTAATGACGTTAATGGAGTCGTTAATGAGTTGTGCGATCAAGGATCC 174
                                                                                                                                                               CAACACCCTGCTTCAAGGTTACTCCGGGATCAGATTTTGAGATCCTAGAAGCCATTTACCAA 694
                                                                                                                                                                                                                                                                                           AACGGAAACAAGCCACACTTTCCACATTTCAGCCACCAGAGCCGCCATIGATTCGTCAGAAT 594
                                                                                                                                                                                                                                                                                                                                                                                                                AGGCGGTGCTCCAGAAGGAGCTTAFTAGGTTTCTGAATGCTGGAATCTTTGGGGAATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGGCGGTGCTTTACAGAAGAGCTCATTAGATTTTTGAACGCCGGAATATTCGGCAATGG 534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AACTGATTACGGCGTCACCACCGGTTTTTGGTGCCACTTCTCATCGGAGGACTAAACA 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AACTGATAGTTATIGGTGTCACCACCGGCTTCGGGCGCCACCTCTCACCGGAGAACTAAGCA 474
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTTGAATTGGGGAATGGCAGCCGATTCGTTGAAAGGAAGCCATTTAGATGAAGTTAAACG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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KGTUSYGVTTGFGATSHKFTKQGGALQKELIFFLNAGIFGNGTESSHTLPHSATRAAM
LVRINTLLQGYSGIREEILEAITKFLNHNITPCLFLRGTITASGDLVPLSYIAGLLTG
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NTI, AVI, SEVI, SATFAEVMNGKPEFTDHI, THKI, KHHPGOTEAAATMEH I LDGSGYVKAA
HKI, HEMDPI, OK PKQDRYAT, RTSPOWI, GPOTEVTRSATKMTERET INSVNDNPT, I DVSRN
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/protein_id-"BAA95629.1"
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                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trachcophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      phenylalanine ammonia-iyase Stylosanthes humilis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Stylosanthes humilis
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                                                    /gene="PAL17.1"
32. .2179
                                                                                                                                                                                                            /organism="Stylosanthes humilis"
/strain="Paterson"
                  /gene-"PAL17.1"
/EC_number="4.3 1.5"
                                                                                                                                                                                                                                                             Location/Qualifiers
/codon_start-1
                                                                                                     /gene-"PAL17.1"
                                                                                                                                     /gene-"PAL17.1"
                                                                                                                                                           /tissue_type="stem"
1. .2428
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753 GAATOGGATOGGACTTOTTTGAGTTGCAAOOTAAAGAAGGCCTTGCACTGGTGAATGGCA
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                                                                            GAGTIGAAGGTGGGTTCTTCGAGTTACAGCCGAAAGAAGGGGCTAGCACTTGTTAACGGCA 887
                                                                                                                                                                                                                                                                                                            CCTCTGGTGACCTTGTTCCATTATCATATATTGCTGGTTTGTTAACCGGCAGACCAAATT
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LKTLLPKEVEGARIAYENGOSAIPNKIKECRSYPLYKEVREELGTEMLTGEKVRSPGE
ECDKLETAMCQGKIIDPLLECIGEWNGAPLPLC"
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ALHGGRYOGTPIGVSMONTLAVASIGKLMFAQFSELVMDYYNGLPSNLSASRRPSL
DYGFROTEINAASYGSELOYLANDYSHVOSAROHNODVNSLGALISABYINEAVEILK
LMSPTYLIALOQAIDLRHLEENLKNTVKNTVSQVAKRTLTTGVNGELHPSRFGEKDLL
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GTDSYGVTTGFGATSHRRTKQGGALQKELIRFLNAGIFGNGTEINCTLPHTATRAML
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/protein_id="AAA99500.1"
/db_xref="G1:55642"
/translation="MDTHANADATFCLTANNGOOPRHDPLNWAAAAFALKGSHLDEVK
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TCCAACAACAATTCAAACTTCCTCTTACCCAAACAACTTCAACCTCTTACAATCCCTTATG 2027
                                                                                                                                                                                                 CTTIGGAGTGCTACGTACCCTTTIGATGCAGAAGCTAAGGCAAGTTTTTTGGTGGAACATGCAC 1832
                                                                                                                                                                                                                                                                                                                                GTGAGAAGGATCTTCTCAAGATEGTTGATAGGGAGTATTGCTTTGCATACATACATCATC 1772
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                                                                  TTGCAAATGCTGAAAATGAGAAGAATGTGAAACACCTCAATCTTCCAGAAAATTACAAACCT
                                                                                                                              TAMACANCIGICGANACIGGAIGANGANGACACTANGACCTCCATCTTCCAAAAGGATCGCTAGCT 1967
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KAVGDNGESLANAGOAFKLAGANSGLEFELOPKEGLALVOTAVGSGLASIALVEAN IL
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ORIGIN BASE COUNT Matches 1629; Conservative Query Match 1015 ACTGATCACCTGACGCACAAGTTGAAGCATCACCCGGGCCAAATAGAGGCAGCCGCTATA 1074 1004 ACCGATCACTTGACACACAAATTGAAGCATCACCCTGGTCAAATCGAGGCGGCGGCGGCGATC 1063 715 GCATCAGGCGATCTCGTGCCCTTATCCTACATCGCAGGCCTCTTAACGGGTCGGCCCAAC 774 655 ATCACCAAATTCCTCAATCACAACATCACCCCATGCTTGCCCCTCCGCGGGACCATAACC 595 475 ACGAAACAAGGCGGTGCTCTTCAGAAGGAGCTTATTAGGTTCTTGAACGCCGGAATATTC 534 407 AATAAAGGAACTGATAGTTATGGTGTCACCACCGCGCTTTCGGCGCACCTCTCACCGGAGA 466 181 AATGATCCCTTGAACTGGGTGGCGGCGGCGGAGGAGCTGAAGGGGAGCCATCTGGATGAG 240 167 AAGGATCCATTGAACTGGGGAGTTGCAGCGGAGGCGTTGACCGGAAGTCACCTTGATGAG 226 944 TTGTTGTCGGAAGTGTTATCGGCGATCTTCGCTGAGGTTATGCAAGGGAAGCCGGAGTTT 1003 895 GGGACAGCTGTTGGGTCCGGATTGGCCCTCAATTGCCCCTTTATGAAGCGAACATCCTTTCC 767 TCCAAAGCCGTTGGCCCCACCGGAGAAGTCCTCAATGCCGAAAAGGCCCTTCGCTGCAGCC 647 ATCACCAAGTTCCTTAACAACAACATCACCCCTTGTTTACCCCCTCCGTGGAACCATCACC 706 535 GGAAATGGGACAGAATCTACGCACACACTGCCACATTCAGCAACCAGAGCAGCAATGCTT 594 355 CTGGCGGAGTCATCGCGTGCTGGGGTGAAGGCCAGCAGTGATTGGGTGATGGAGAGCATG 414 301 241 GTGAAGCGGATGGTGGAGGAGTTCAGGAAGACAGTGGTGAAGCTCGGCGGCGAGACTCTG 300 Local Similarity GGAG---TEGAAGGTGGGTTCTTCGAGTTACAGCCGGAAAGGAGGGCTAGCACTTGTTAAC 883 ACTAAGCAAGGCGGTGCTTTACAGAAGGAGCTCATTAGATTTTTGAACGCCGGAATATTTC CTGTCGGAAGCCGCGAGGGCTGGAGTTAAGGCGAGTAGTGATTGGGTTATTGGAGAGCATG 406 GGCACCGCCGTGGGGTCCGGGATGGCTTCCATGGTTCTATTTGATGCTAATGTACTTGCG 943 TCCAAGGCCGTGGGGCCCAACGGCGAGTCCCTCAATGCGGAACAAGCATTCAAGCTTGCC GTGAGAATTAACACCCTCCTCCAGGGATACTCCGGCATCAGATTTGAAATCTTGGAAACC GTCAGAATCAACACCCTCCTCCAGGGTTACTCCGGCATCCGATTCGAGATCTTGGAAGCC 646 ACGATATCTCAGGTGGCGGCGATCGCCGCTAGGGA------CAATGAGGTGCCCGTGCAG 354 TTGTTGGCTGAAGTGATGTCCGCCGTTTTTGCAGAGGTAATGAACGGGAAAGCCCGAATTC 1014 ACAGTTTCTCAGGTGGCGGGGATCGCAGCTGCTAATGACAGTGACACCGTGAAGGTGGAG GGTGCCAATTCCGGATTATTCTTCGAGTTGCAGCCGAAAGAAGGCCTCGCCCTCGTGAAC GCCTCCGGTGACCTTGTCCCATTATCATACATCGCCGGCCTCTTAACCGGCCGCCCCCAAC 766 GFKGSBLAMASYCSELGFLAREVTNHVQSAEGHNODVASIGILISSRKTVBALDIIKLM SSTYLVALCQALDLPHLEBLIRILSVKNITSOVAKRTLTTYSVAFELHPSPFYELDLLFV VDREYVFAYVUDDPCSATYPLMOKLROVLVEHALKNGENEKNASTSIFOK BEAFFRAEK AVLPKEVESARVALEDGKPAIANRITECRSYPLYKFIREELGTNFLTGEKVMSPGEEG DRVFTAMSKGLIVDPLLKCLEGWNGAPLPIC" 50.6%; 73.1%; 549 c 0; Mismatches 590; Indels Score 1235; DB 8; Pred. No. 4.2e-285; 628 g 587 t Length 2403; 10; Caps 834 Ψ

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2204 THOPTGGAGTGTCTTGGAGGGTGGAATGGGGAACCTCTTCCAATATGTTAGGAAAGTGAG 2263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheo
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Convolvulaceae; Ipomoea.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ipomoca batatas (strain:beniazuma) wounded root cDNA to mRNA
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                                                             603
                                                                                                                                                                                                                                                                           /product-"Phenylalanine Ammonia-Lyase"
/protein_id-"BAA11459.l"
/protein_id-"BAA11459.l"
/db_xref-"GI:1122743"
/trans:latiou-"MEGAIANCHTNIDECIKUDPLNWEMAALSI.KGSHLDEVKRMVAEF
KNPAVKIGGOTUTSLRSPPIAARDNASKWSSPRI.PARRESSSDWVMNSMNNGTDSYGV
TTGFGARTSHRFTKNGHAIQQELIRFLAAGIFGTGTGASHTLIPHSATRAAMI.VRINTLI.
                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xrei="taxon:4120"
/clone="pAL2-8"
/tissue_type="wounded root"
87, .2213
                                                           AVCDGGTIDPLLECLKSWDGAPLPIC"
1 594 c 604 g 595 t
                                                                                                                                                           LOKPKODRYALKTSPOWLGPO LEV LROATKMLEHE LUSVUDUPLLDVSRNKALHGGNF
OGTP LGVSMDUSRLALAS IGKLLFAOF SELVUDYYNUGLPSULTAGRNPSLDYGFKGV
ELAMASYCSELOFLANPYTUHVQSAEOHNODVUSLGLLSARKTAEAVDVLKLMSSTYL
                                                                                                                    VALCQA I DLRIILEENLKNAVRNTVNQVAKRTLTMGVNGELIIPSRFCEKDLLRVVDREY
VFAYADDPCSANYPLFQKLRQVLVDHALQNGEHEKNVSTS I FQK I AAF EDELKAVLPK
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                                                                                                   EVEGARSATENGNPATPNRTTECRSYPLYKEVREELGTEMLTGEKVKSPGEVCDKVFT
                                                                                                                                                                                                                                                              QGYSGIRFEILEAITKLLNIINTTPCLPLRGTITASGDLVPLSYIAGLLTGRPNSKAVG
                                                                                                                                                                                                                                                                                                                                                                                                      /codon_start-1
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Best Local Similarity
Matches 1604; Conser
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                                                                                                                                                                                                                                                                   AAGGCGGCAAAAGGTCCACGAAATGGACCCGITACAGAAAACCAAAAACAAGATCGTTAT 1156
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                                                                           y Match 50.3%;
Local Similarity 72.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Appert, C., Logemann, E., Hahlbrock, K., Schmid, J. and Amrhein, N. Structural and catalytic properties of the four phenylalanine ammonia-lyase isoenzymes from parsley (Petroselinum crispum Ny Eur. J. Biochem. 225 (1), 491-499 (1994)
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Div. Applied Life Sciences; Kitashirakawa, Kyoto, Kyoto 606-01,
Japan (E-mail:yazaki@kais.kyoto-u.ac.]p, Tel:075-753-6384,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; euasterids I incertae sedis; Boraginaceae;
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                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                               LLQGYSGIRFEILEAITKFLNTNITPCLPLRGTITASGDLVPLSYIAGLLTGRPNSKA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FRKPVVQLAGKTLTIGQVAAIAARDDGVTVELAEAAREGVKASSDWVMDSMNKGTDSY
GVTTGFGATSHRRTKQGGALQKELIRFLNAGIFGNGTETSHTLPHSATRAAMLVRINT
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/clone_lib="expression library of Lithospermum cells
/cultured in pigment production medium"
/dev_stage-"dedifferentiated cells"
/note-"Sieb. ct Zucc."
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/protein_id-"BAA24928.1"
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                                                                                                                                                                                                                                                                                                 EYVFAYADDPCLTTYPLMQKLRETLVGHALDNGENEKDVNTS1FHK1A1FEEELKA1L
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        714 CTCCATGCCTACCCCTTCGTGGCACGATCACCGCCTCTGGTGACCTCGTCCCCCTCTCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           534 AACTTATTAGATTCTTGAATGCTGGAATATTTGGCAATGGAACAGAAACTAGCCACACAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALGCCCTCCGTACATCGCCTCAATGGCTTGGTCCTCAGATCGAAGTGATCCGTTCTGCTA
                                                                                                                     ATGCTCTCCGTACATCTCCCCAATGGCTCGGACCTCAAATCGAAGTAATCCGATCATCAA 1214
                                                                                                                                                                                                                                    TCAAGGCGGCGCAAAAGGTCCACGAAATGGACCCGTTACAGAAACCAAAACAAGATCGTT 1154
                                                                                                                                                                                                                                                                                              ATCCAGGACAGATTGAGGCTGCTGCTATCATGGAGCACATTTTGGATGGTAGTGGATATG
                                                                                                                                                                                                                                                                                                                                                         ACCCTGGTCAAATCGAGGCGGCGATCATGGAGTATATTTTGGACGGAAGCGATTACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      {	t TGGTTCTTTATGAAGCCAACATTTTGGCTGTCTTGTCTGAAGTGATCTCGGCTATTTTTCG}
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                                                                                                                                                                            TTAAGGCTGCTCAGAAGTTACATGAGATGGATCCTCTGCAGAAGCCTAAGCAAGATCGTT
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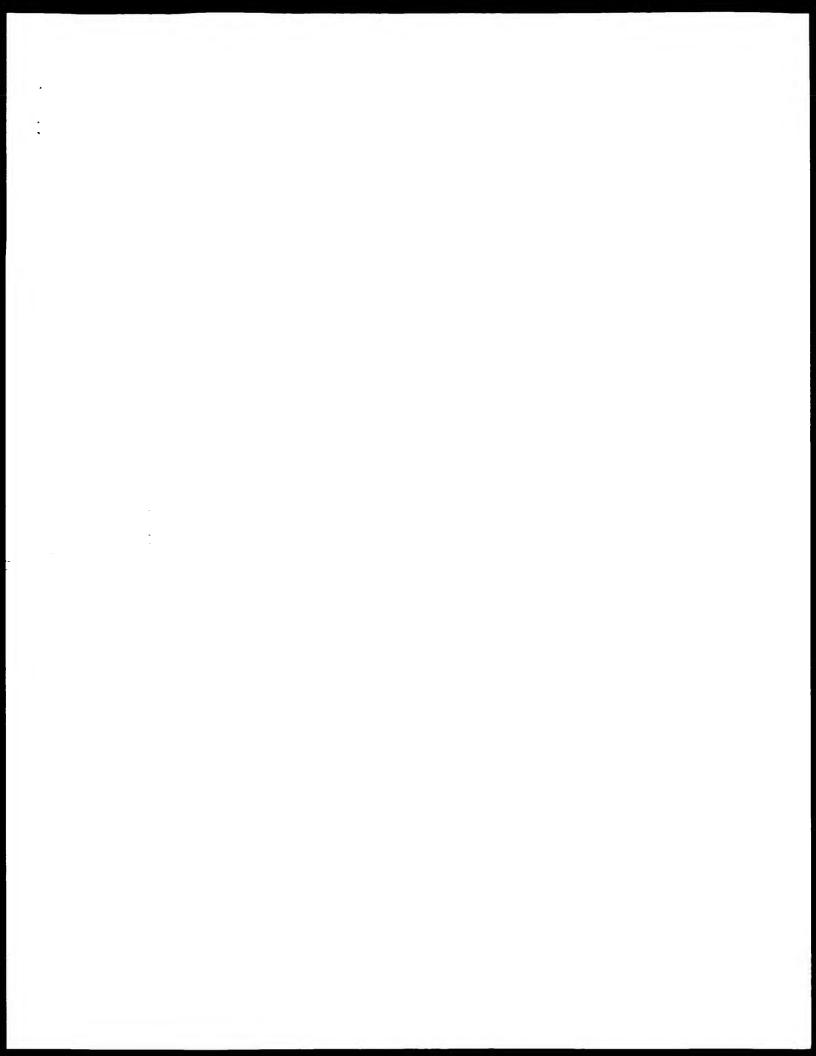
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Search completed: March 28, 2003, 23:39:52 Job time : 6255 secs



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ALIGNMENTS

source	FEATURES	JOURNAL	TITLE	AUTHORS	JOURNAL		TITLE		AUTHORS	REFERENCE			ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	LOCUS	AY103647	RESILT 1
/	Location/Qualitiers	Submitted (25-APR-2002) Maire Mapping Project, University of Missouri, Columbia, MO 65211, USA	Direct Submission	2 (bases I to 2598)	Unpublished (2002)	Overgo Probes	Maize Mapping Project/DuPont Consensus Sequences for Design of	Arthur, L.W., Hanafey, M., Morgante, M. and Tingey, S.V.	Hainev.C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitsitt.M.S.,	1 (bases 1 to 2598)	clade; Panicoideae; Andropogoneae; Zea.	Eukaryöta, Viridiplantae: Streptöphyta: Embryophyta: Tracheophyta: Spermatöphyta: Maddollöphyta: Liliopsida: Phales: Poaceare: PACC	Zea mays	Zea mays.	HTC.	AY103847 1 G1+21208725	AY103647	PCol42084 mRNA sequence.	AY103647 2598 bp mkNA linear HTC 25-MAY-2002		

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ORIGIN
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1010 САСТТВАСАСАВААТТВААВСАТСАВСЕТВВТСААДТЕВАВСЬЭВ ЭЭВЭВВЕВАТСАТВВАВ 1059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           470 AAGCAAGGCGGTGCTTTACAGAAGGAGCTCATTAGATTTTTGAACGCCGGAATATTCGGC 529
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                                                                                                                                                  TCGGAAGTGTTATCGGCGATCTTCGCTGAGGTTATGCAAGGGAAGCCGGAGTTTACCGAT 1009
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Library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2171 GAGTGCCT/MGGAGGGGAGGGAGGGAGCGGCTGCCCAT 2208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2210 GAGTGTCTTGGAGGGTGGAATGGGGAAACCTCTTCCAAI 2247
                                                                                                                                         218
                                                                                                                                                                                                    434 ACCACCGCTTTCCCCCCCCCCCCCCCCGGAGACTAAGCCAAGGCGGTGCTTTTACAGAAG 493
335 TACTCCGGCATOGCTTCGAGATCCTCGAGGCCATCACCAAGCTCATCAACAACACCGGCGTC
                                614 TACTICCGGCATTCCGATTCGAGATCTTGGAAGCCATCACCAAGTTCCTTAACAACAACATC 673
                                                                                    554 CTTCCACATTCAGCCACACAGGCGGCACAGACATGATGAGAATCAACACCCTCTCTCCAGGGT 613
                                                                  275 CTCCCGTCCGAGGTTTCGCGTGCGGCCATGCTCGTCCGCATCAACACCCTCCTCCAGGGC 334
                                                                                                                                                                                                                                                                                                         374 AAGAGAATAGTGATTGATTATGAAGAAGAAGAAAGGAACTGATAGTATGGTGTC 453
                                                                                                                                                                                                                                                                           98 ATGGCGAGCAACACGCCATCCTGGACTGCATCGCCCACGGCGGCGACATCTACGGCCGTC 157
                                                                                                                                                                      GAGCTCATTAGATTTTTTGAACGCCGGAATATTTCGGCAATGGAACGGAAACAAGCCACACA 553
                                                                                                                                 GAGCTGCTCAGGCATCTCAATGCCGGGATCTTCGGCAACGGCTCCGA---CGGCCACACG 274
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Zea mays
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (25-APR-2002) Maize Mapping Project. University of Missouri, Columbia, MO 65211, USA
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Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V.
Maize Mapping Project/DuPont Consensus Sequences for Design of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCGAAAGAAGTTGAAGGTGTTAGAAATCGCTTATGAGAATGATACATTGTCGATTCCAAAC 2053
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                                                                                                                                                                                                                                                Department of Vegetable Crops, R.W.Michelmore Lab University of California at Davis (UCD) Asmundson Hall, UCD, Davis, CA 95616, USA
                                                                                                                                                                                                                                                                                                                                                            Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                    Lin,H., van Damme,M., Lavelle,D., Chevalier,P., Ziegle,J., Ellison,P., Kolkman,J., Slabaugh,M.S., Livingston,K., Zhou,Y., Lai,Z., Church,S., Jackson,L. and Bradford,K.
Lettuce and Sunflower ESTs from the Compositae Genome Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta, Embryophyta, Tracheophyta, Spermatophyta; Magnoliophyta, eudicotyledons, core eudicots; Asteridae; euasterids II; Asterales; Asteraceae; Lactuceae;
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                                                                                                                                                Email: akozik@atgc.org [michelmore@vegmail.ucdavis.edu] belongs to contig QG_CA_Contig6760, see http://cgpdb.uc
                                                                                                                                                                                                                                                                                                                              Contact: Alexander Kozik [R.W.Michelmore]
                                                                                                                                                                                                                                                                                                                                                                              http://compgenomics.ucdavis.edu/
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                                                                                                                                                                                                   Fax: 1-(530)-752-9659
                                                                                                                                                                                                                                Tel: 1-(530)-742-1742
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                                                                                                                          1429 TCTCTCCGGTGGACGTAACCCTAGTTTGGACTACGGGTTCAAAGGTGGAGAAATCGCCAT 1488
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                                                                                             541 CATGTTCGCTCAATTTTCTGAGCTGGTTAACGATTCTACAACAATGGATTACCATCGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         421 CGACAACCCATTGATCGACGTTTCCAGAAACAAAGCTTTACACGGTGGTAACTTCCAAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 TCACTTGACACACACATTGAAGCATCACCCTGGTCAAATCGAGGCGGCGGCGATCATGGA 240
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TAG_LIB=OG_ABCDI lettuce salinas
TAG_TISSUE-chemical induction
TAG_SEO=TGTAGCCGGG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          size bias. Details of each source of RNA and library
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                                                                                                                                                                      TTGATGCTAATGTACTTGCGTTGTTGTTGGCAGAAGTGTTATCGGGGGAATCTTCGCTGAGGTTA 983
                                                                                                                                                                                                                                                                                                                                                                   GCCTCATCACGGGCCCCCACAAACTTCGGTGGTGGGGTGGGCGACGACGGCAGGAAGGTGGGCG
                                                          AGGGCCTCGCCATIGGTTCAACGGCACCGCCGTGGGGCTTCCGGCCTTCGACCGTGCTCT
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                                                                                                                                    TICGAGGCCAACGTTICTICGCCGTICATIGGCCGAGGTCATICTICGGGGGGTGTTTCTTGCGAGGTTCA
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Spermatophyta, Magnoliophyta, Liliopsida; Poales, Poaceae; PACC
Clade, Panicolabae, Andropopourae, 25a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zea mays PCO142078 mRNA sequence. AY104679
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Department of Vegetable Crops, R.W.Michelmore Lab
University of California at Davis (UCD)
Asmundson Hall, UCD, Davis, CA 95616, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          http://compgenomics.ucdavis.edu/
Unpublished (2002)
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Lettuce and Sunflower ESTs from the Compositae Genome Project
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Lin,H., van Damme,M., Lavelle,D., Chevalier,P., Ziegle,J., Ellis
,P., Kolkman,J., Slabaugh,M.S., Livingston,K., Zhou,Y., Lai,Z.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Alexander Kozik [R.W.Michelmore]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae, Streptophyta, Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: akozik@atyc.ory [michelmore@veymail.ucdavis.edu]
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TAG_TISSUE=leaves dark grow
TAG_SEQ=GCTAGTCGGG"
                                                                                                                                                                                                                                                                                                                                                                                      transformations made with four size classes to minimize size bias. Details of each source of RNA and library construction can be obtained at http://capdb.ucdavis.edu/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       source of RNA. eDNAs were then pooled, size-fractionated, directionally cloned into a custom medium-copy vector and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note-"Vector: pBRcDNASSIAB; The library was constructed from 10 different sources of RNA from a single genotype. Separate cDNAs were generated using primers that incorporated unique 5' and 3' tays to distinguish each
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                                                                          Kozik,A., Michelmore,R.W., Knapp,S., Matvienko,M., Rieseberg,L., Lin,H., van Damme,M., Lavelle,D., Chovalier,P., Ziegle,J., Ellison,P., Kolkman,J., Slabaugh,M.S., Livingston,K., Zhou,Y., Lai,?., Church,S., Jackson,L. and Bradford,K.

Lettuce and Sunflower ESTs from the Compositae Genome Project http://compgenomics.ucdavis.edu/
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Department of Vegetable Crops, R.W.Michelmore Lab
                         Contact: Alexander Kozik [R.W.Michelmore]
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                          930 CTAATGTACTTGCGTTGTTGTCGGAAGTGTTATCGGCGATCTTCGCTCACCTTATCCAAG 989
                                                                                                                                                                                                                                                                                                                                                                                  399
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579 CTAATGTAVITGGGTTGTTGTGGGAAAGGTTATGGGGGATGTTGGGTGAGGTTATGCAAG 638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     510 TGAACGCCGGAAATATTCGGCAATGGAACGGAAACAAGCCACACACTTCCCACACTTCAGCCA 569
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Plate: QGH9 row: N column: 08.
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Asmundson Hall, UCD, Davis, CA 95615, USA
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belongs to contiq QG_CA_Contig6760, see http://cgpdb.ucdavis.edu/
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Fax: 1-(530)-752-9659
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/clone-"QGH9NO8"
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/lab_host="E.coli"
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98.8%;
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- 830 - GTTGAAGGTGGGTTGTTCGAGTTACAGCGGAAAGAAGAGCTAGCACTTGTTAACGGCACC - 889

Matches

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28.48; 99.78;

Score 694.4; DH 1 Pred. No. 6.7e-82; Mismatches

DH 14; Length 710;

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Best Local Similarity

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Contact: Alexander Kozik {R.W.Michelmore}
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Lin,H., van Damme,M., Lavelle,D., Chevalier,P., Ziegle,J., Ellison
,P., Kolkman,J., Slabaugh,M.S., Livingston,K., Zhou,Y., Lai,Z.,
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Plate: QGD5
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belongs to contig QG_CA_Contig6760, see http://cgpdb.ucdavis.edu/
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                                                                           TAC_SEQ+TGTAGCCGGG"
                                                                                                                         construction can be obtained at http://cgpdb.scdavis.edu/
TAG_LIB-QG_ABCDI lettuce salinas
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                                                                                                                                           Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L.
Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegle, J., Elli
P., Kolkman, J., Slabaugh, M.S., Livingston, K., Zhou, Y., Lai, Z.,
                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids II; Asterales, Asteraceae, Lactuceae;
                                                                                                                                                                                                                                                                                                                      Lactuca sativa
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EST.
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Department of Vegetable Crops, R.W.Michelmore Lab University of California at Davis (UCD)
                                       Contact: Alexander Kozik [R.W.Michelmore
                                                              Unpublished (2002)
                                                                                  http://compgenomics.ucdavis.edu/
                                                                                                        Church, S., Jackson, L. and Bradford, K.
Lettuce and Sunflower ESTs from the Compositae Genome Project
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1370 ATGTTGGCTCAAFIFICIGAGCIGGIIAACGATIFCIACAACAAFGGAFIACCAICGAAF 1429
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541 ATGTTCGCTCAATTTTCTGAGCTGGTTAACGATTTCTACAACAATGGATTACCATCGAAT 600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 CACTTGACACACAAATTGAAGCATCACCCTGGTCAAATCGAGGCGGCGGCGATCATGGAG
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Local Similarity 99.2%;
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Tel: 1-(530)-742-1742
Fax: 1-(530)-752-9659
Email: akcolk@atgc.org [michelmorc@vegmail.ucdavis.edu]
belongs to contig OG_CA_Contig6760, see http://cgpdb.ucdavis.edu/
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TAG_LIB+QG_ABCDI lettuce salinas
TAG_TISSUE=chemical induction
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/cultivar="Salinas"
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Department of Vegetable Crops, R.W.Michelmore Lab
University of California at Davis (UCD)
Asmundson Hall, UCD, Davis, CA 95616, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QGG18805.yg.abl QG_EFGHJ lettuce serriola Lactuca sativa cDNA clone QGG18805, mRNA sequence.
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Lettuce and Sunflower ESTs from the Compositae Genome Project

http://compgenomics.ucdavis.edu/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: 1-(530)-742-1742
Fax: 1-(530)-752-9659
Email: akozik@atgc.org [michelmore@vegmail.ucdavis.edu]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (2002)
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                                                                                                                                                                                                                                                                                                                                                                                               183
                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                              construction can be obtained at http://cgpdb.ucdavis.edu/
TAG_LIB-QG_EFGHJ lettuce serriola
TAG_TISSUF-leaves dark grow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Separate cDNAs were generated using primers that incorporated unique 5' and 3' tags to distinguish each source of kNA. cDNAs were then pooled, size-fractionated, directionally cloned into a custom medium-copy vector and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      transformations made with tour size classes to minimize size bias. Details of each source of RNA and library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note-"Vector, pBRcDNAStiA3; The library was constructed from 10 different sources of RNA from a single genotype.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /cultivar-"L.serriola'
/db_xref-"taxon:4236"
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Contact: Alexander Kozik (R W Michelmore)
Department of Vegetable Crops, R W Michelmore
University of California at Davis (UCD)
Asmundson Hall, UCD, Davis, CA 95616, USA
Tel: 1-(530)-742-1742
Fax: 1-(530)-752-9659
                                                                                                                                                      Kozik,A., Michelmore,R.W., Knapp,S., Matvienko,M., Rieseberg,L.,
Lin,H., van Damme,M., Lavelle,D., Chevaller,P., Ziegle,J., Ellison,P., Kolkman,T., Slabaugh,M.S., Livingston,K., Zhou,Y., Lai,Z., Church,S., Jackson,L. and Bradford,K.
Lettuce and Sunflower ESTs from the Compositae Genome Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HQB59819 661 bp mRNA linear EST 15-AUC-200
QCD7821.yg.ab1 QC_AHCD1 lettuce salinas Lactuca sativa chwa clone
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601 GCTAGCACTFOFFAACGGCACCGCCGTGGGGFCCGGGATGGCTTCCATGGTTCTATF 657

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BASE COUNT
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tor details.
Plate: QGD7
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TAG_TISSUE-chemical induction
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/cultivar-"Salinas"
/db_xref-"Laxon:4236"
/clone-"QGD7E21"
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                                                   121 GGAGAACGGTAATCACGTTAATGGAGTCGTTAATGAGTTGTGCATCAAGGATCCATTGAA 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Department of Vegetable Crops, R.W.Michelmore University of California at Davis (UCD) Asmundson Hall, UCD, Davis, CA 95616, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Alexander Kozik [R.W.Michelmore]
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Kozik,A., Michelmore,R.W., Knapp,S., Matvicnko,M., Ricseberg,L.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: 1-(530)-742-1742
Fax: 1-(530)-752-9659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     http://compgenomics.ucdavis.edu/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: akozik@atgc.org [michelmore@vegmail.ucdavis.edu]
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Lin,H., van Damme,M., Lavelle,D., Chevalier,P., Ziegle,J., Ellison,
P., Kolkman,J., Slabaugh,M.S., Livingston,K., Zhou,Y., Lai,Z.,
                                                                                                                                                     University of California at Davis (JCD)
Asmundson Hall, UCD, Davis, CA 95616, U
Tel: 1-(530)-742 1742
Fax: 1-(530)-752-9659
                                                                                                                                                                                                                                                            Contact: Alexander Kozik [R.W.Michelmore
                                                                                                                                                                                                                                                                                     Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; cudicotyledons; core eudicots; Asteridae; euasterids II; Asterales, Asteraceue, Lactuceae;
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                                                                                                                                                                                                                                          Department of Vegetable Crops, R.W.Michelmore Lab
                                                                                                                                                                                                                                                                                                        http://compgenomics.ucdavis.edu/
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Lettuce and Sunflower ESTs from the Compositae Genome Project
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                                                                                                         belongs to contig QG_CA_Contig6760, see http://cgpdb.ucdavis.edu/
                                                                                                                            Email: akozik@atgc.org [michelmore@vegmail.ucdavis.edu]
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BQ865594 LUCUS DEFINITION ACCESSION

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QGC5F22.yg.abl qd_ABCDI lettuce
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Best Local Similarity 96.9%;
                                                                                                                                                                                                                                                                                                                   1360 CGGANAACTCATGTTCGCTCAATTTTCTGAGCTGGTTAACGATTTCTACAACAATGGATT 1419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1300 CHICCAAGGAACCCCAAFCCGAGFTFCCATGGACACACCCGFCTCGCCAFTGCTGCAAT 1359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | 1180 | SYTYOGACCTYANATYGANGTANTSCHATYANYANAYANAATGATYGAYAGGGANATYAN | 1239
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601 ACCATCGAATCTCTCCGGTGGACCGTAGCCTAGTIGGATTACAGGTTCAAAGGT 655
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                                                                                                                                                                                                           541 TGGAAAACTCATGGTCGCTCAATTTTCTGAGCTGGTTAACGATTTCTACAATAATGGATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 GTTTTACCGATCACTTGACACTCAAATTGAAGCATCACCCTGGTCAAATCGAGGCGGCGGC
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                                                                                                        ACCATCGATCTCTCCGGTGGACGTAACCCTAGTTTGGACTACGGGTTCAAAGGT 1474
                                                                                                                                                                                                                                                                                                                                                                                                                           CTTCTAAGGAACCCCAATCGGAGTTTCCATGGACAACACCCGTCTCGCCATTGCTGCCCAT 540
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         635; Conservative
                                                                                                                                                                                                                                                                 175 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            directionally cloned into a custom medium-copy vector and transformations made with four size classes to minimize size bias. Details of each source of RNA and library construction can be obtained at http://egpdb.ucdavis.edu/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TAG_SEQ-Not found"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Separate cDNAs were generated using primers that incorporated unique 5' and 3' tags to distinguish each
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /cultivar-"L.serriola"
/db_xref-"taxon:4236"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   source of RNA, cDNAs were them pooled, size-tractionated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       from 10 different sources of RNA from a single genotype.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note-"Vector: pBRcDNASfiAH; The library was constructed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="QGG27H21"
/clone_lib="QG_EFGHJ lettuce serriola"
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 Mismatches

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Pred. No. 1.5e-72;
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                                                      GGTTACTCCGGCATCCGATTCGAGATCTTGGAAGCCATCACCAAGTTCCTTAACAACAAC 670
                                                                                                            ACACTTCCACATTCAGCCACAAGAGCAGCCATGCTTGTCAGAATCAACACCCTCCTTCAA 241
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University of California at Davis (UCD)
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Lettuce and Sunflower ESTs from the Compositae Genome Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact Alexander Kozik [F W Michelmore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (2002)
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1-(530)-752-9659
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Department of Vegetable Crops, R.W.Michelmore
University of California at Davis (UCD)
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Lettuce and Sunflower ESTs from the Compositae Genome Project
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Fax: 1-(530)-752-9659
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                                                                                                                                                                                                                                                                                                                                                                                              Email: akozik@atgc.org [michelmore@vegmail.ucdavis.edu]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lactuca sativa.
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/note-"Vector: pBRcDNASfiAB; The library was constructed from 10 different sources of RNA from a single genotype. Separate cDNAs were generated using primers that incorporated unique 5' and 3' tags to distinguish each
                                                                                                                                 /clone="QGH13K13"
/clone_lib="QG_EFGHJ lettuce serriola"
                                                                                                                                                                                       /db_xref="taxon:4236"
                                                                                                                                                                                                                 /cultivar="L.serriola"
                                                                                                                                                                                                                                          /organism="Lactuca sativa"
                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                        /lab_host="E.coli"
                                                                                                                                                                                                                                                                                                                     row: K column: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              711 bp
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                                      ORGANISM
                                                                                                                                                                                                                                                                                                                                                           670
                                                                                                                                                                                                                                                                                                                                                                              871 A3CACTTGTTAACGGCACCGCCGTGGGGTCCGGGATAGGTTC 912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 811 GGCCTTCGCTGCAGCCGGAGTTGAAGGTGGGTTCTTCGAGTTACAGCCGAAAGAAGGGCT 870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        511 GAACGCCGGAATATTCGGCAATGGAACGGAAACAAGCCACAGACTTCCACATTCAGCCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          331 CACCGTGAAGGTGGGATGCTGTCGGAAGGCGGGAGTTGGAGTTAAGGGGAGTAGTGATTG 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             271 COCACGAGAGACACTITACACTITETEAGGIGGEGGGGAICSCAGCIGCIAAIGACAGIGA 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   211 AAGTCACCTTGATGAGGTGAAGAAGATGGTTGCGGAGTTCAGAAAGCCGGTGGTGAAGCT 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10 ATGGCCGCTT4AC4G4GGCACACACAATGGTGAACGAGTTCAGGAAGCCTGCTGTTGTGAAGCT 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGTTATGGAGAGGATGAATAAAGGAACTGATAGTTATGGTGTCACCACCGGCTTCGGCGC 450
                                                                                                                                                                                                                                                                                                                                                        ACCACTTGTTAATGGCACCGCCGTCGGATCTGGGATGGCTTC 711
                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGCCTTCAATTTCGGAGGAGTTACTGGTGGGCTCTTTGAGCTACAACCTAAAGAAGGTCT 669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CACCGGCCCCCCAACTCCCAAAGCAGTCGGCCCCAAGGGTGAAATCCTCAACGCCGAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AACCGGCCCCAACTCCAAAGCCCTTGGCCCCACCGGAGAAGTCCTCAATGCCGAAAA 810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | COSTAGAACOATOMOOSCOTOOOSGIGACOTIGEOCSATTATOATOATOAGOGGGGGGTT 750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | CGAGATC1||GGAAGCTA+CACCAAG++CCTTAACAACAACATCACCCCTTTGTTTTACCCCTT|| 690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAACGCCGGAATNITTTGGCAACGGAACGGAATCAAGCCACACCCTTTCCGCATTTCAGCAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CACTGTGAAGGTGGAGCTGTCGGAGACTGCTATGGCTGGAGTGAAAGCGAGTAGTGATTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCGAGGAACAATCACCGCCTCCGGCGACCTTGTCCCCATTGTCTTACATCGACGGACTTCT
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                                                                                                                                         OHF4e07.yg.abl QH_EFGHJ sunflower RHA280 Helianthus annuus cDNA clone OHF4e07, mkNA sequence.
Helianthus annuus
Eukaryota; Viridiplantae, Streptophyta, Embryophyta; Tracheophyta;
                                                                                          EST.
                                                                  common sunflower.
                                                                                                                 BU024517.1 GI:22460937
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                                                         821 GCAGCGGAGTTGAAGGTGGGTTCTTCGAGTTACAGCGGAAAGAAGAGGGTAGCACTGTT
                                                                                                                                                                             241
                                                                                                                                                                                                                           761 CCCANTECAMACCUTTOGECEACGEINGANTECTEMATECEINAMAGECCTTCSCT 820
                                                                                                                                                                                                                                                                                                                                                 701 ATCACCGCCTCCGGTGACCTTGTCCCATTATCATACATCGCCGGCCTCTTAAGCGGCCGC 760
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   521 ATATTCGGCAATGGAACGGAAACAAGCCACACTTCCACATTCAGCCACAGCCGCC 580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 ATGTTGGTCAGAATCAACACCCTCCTCCAGGGATAFTCCGGCATAAGATTCGAAATCFTG 120
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                                                                                                                                                                       CCCAACT CAAAGGCAGT TGGCCCGGGCGGTGAAGTTGTCAATGCGGGAATCCGCATTCGCC
                                                                                                                                                                                                                                                                                       ATCACCGCTCCGGTGACCTCGTCCCGTTGTCCTACATCGCGGGTCTCCTCACCGGCCGA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             588; Conservative
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Rozik, A., Michelmore, R. W., Knapp, S., Matvienko, M., Rieseberg, L., Lin, H., van Damme, M., Lavelle, D., Chevaller, P., Ziegle, J., Ellison, P., Kolkman, J., Slabaugh, M.S., Livingston, K., Zhou, Y., Lai, Z., Church, S., Jackson, L. and Hradford, K.
Lettuce and Sunflower ESTs from the Compositae Genome Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 for details.
Plate: QHF4 row: e column: 07
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Asmundson Hall, UCD, Davis, CA 95616, USA
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Asteridae; enasterids II; Asterales; Asteraceae; Asteroideae;
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belongs to contig QH_CA_Contig3142, see http://cgpdb.uc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: 1-(530)-742-1742
Fax: 1-(530)-752-9659
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Alexander Kozik [R.W.Michelmore]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (2002)
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/lab_host="E.coli"
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- δÃ Бþ Ŷ Ŷ Qy da γQ Дb Ъ В В 1181 CTCGGACCTCAAATCGAAGTAATCCGATCATCAAC 1215 1121 ATGGACCCGTTACAGAAACCAAAACAAGATCGTTATGCTCTCCGGTACATCTCCCCCAATGG 1180 601 ATGGACCCGTTACAAAAACCAAAAACAAGACGTTACGAGGCTCAGGAGGTCACGTCAATGG 650 361 AATGGTACCGCGGTGGGGTCCGGGGTCCATGGTCTTGTTTTGAAGCCAATGTACTT 420
- Search completed: March 29, 2003, 00:34:00
 Job time : 3134 secs

GenCore version 5.1.4_p5_4578

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Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Published_Applications_NA·*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Copyright (c) 1993 - 2003 Compagen Ltd.
                                                                                                                             /cgn2_6/ptodata/1/pubpna/US09_NEW_FUB.scq:*
/cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
                                                                                                                                                                                                                                                       /cgn2_6/ptodata/1/pubpna/USU6_NEW_PUB.Scq:*
/cgn2_6/ptodata/1/pubpna/USO6_PUBCOMB.scq:*
/cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB seq:*
/cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB seq:*
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                                                                                                                                                                                          /cgn2_6/pt.odata/1/pubpna/US08_NEW_PUB.seq:*
/cgn2_6/pt.odata/1/pubpna/US08_PUBCOMB.seq:*
                           /cyn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
/cyn2_6/ptodata/1/pubpna/US10_PUBCOMB seq:*
/cqn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result

Query

NC.	Score	Match	Match Length DB	EH	ID	Description
_ :	2442	100.0	2442	: و	US-09-964-992A-3	Sequence 3, Appli
رء	1603 B	6 - 7	2380	د	115-09-964-992 A-4	Sequence 4, Aprili
w	1208.8	49.5	2154	9	US-09-938-842A-813	Sequence 813, App
4	1203.2	49.3	2178	9	US-09 938-842A-1713	Sequence 1713, Ap
ſΛ	549.6	12 12 5	912	10	US · U9 · 854 · 122 · 46	Sequence 46, Appl
J)	270.6	11.1	660	10	115-09-770-149-476	Sequence 476, App
7	265.6	10.9	2163	10	IIS-09-939-408A-29	Sequence 29,
3 0	256	10 5	2475	10	IIS-09-939-408A-20	
4	244	10.0	2419	10	US-09-939-408A-12	
10	877	٠ *	2787	10	16 - A804 - 484 - 40 - 811	
=	223.4	9.1	2061	10	US-09-765-873A 31	Sequence 31,
12	223 4	د 1	2151	10	US-09-765-873A 7	Sequence 7, Appli
13	221.8	9.1	2439	10	115-09-939-408A-18	
14	220.2	9.0	2151	10	US · 09 · 765 · 873A · 9	
15	198.8	8.1	363	10	US-09-878-574-3252	
16	171.4	7.0	278	10	US · 09 · 878 · 574 · 10900	
17	169.6	6.9	332	Ę	US-U9-878-574 2410	
18	155.6	5.4	2311	10	US-09-939-408A-14	
19	126	رء د.	279	10	US-09-A78-574-7623	

66, Appl	Sequence	US-09-739-254-66	10	564	2	ń.	45	
11234, A	Sequence	US-09-960-352-11234	10	419	دع س	55	44	
9335, Ap		HS-09-960-452-9335	10	380	K.	55.4	4 4	
4584, Ap	Sequence	US-09-960-352-4584	10	416	2.3	55.8	42	
8414, Ap	Sequence	US-09-960-352-8414	10	312	2.3	55.8	41	C
7419, Ap	Sequence	US-09-960-352 7419	10	377	2.3	56	40	C
12673, A	outletibes	US-09-960-352-12673	10	277	2	56.4	39	
11930, A	Sequence	08-09-460-352-11430	_	Res		2	â	7
11699, A	authatibas	IIS-09-960-352-11699	_	216		56.8	٦7	2
6783, Ap	Sequence	US-09-878-574-6783	_	250		58.8	ن د	
4838, Ap	Sequence	US-U9-294-093H-4838	_	300	2.5	6U	35	
15014, A	Sequence	US-09-960-352 15014	10	375	2.5	60.2	34	
11218, A	oottethes;	ПS-09-960-352-11218	_	424	د ا ار	41	ند	7
7987, Ap	Sequence	US-09-815-242-7987	10	1530		61.8	ندا د ۱	
9335, Ap		5886 358 036 60 SA	ū	X:	F.	£.	3.1	O
12673, A	Sequence	US-09-960-352-12673	10	277	2.6	63	30	С
579, App	Sequence	US-114-770-696-579	į	1 45	2.7	ታን ጎ	29	3
8806, Ap	Sequence	US-09-878-574-8806	10	267	3.4	82.2	28	
7670, Ap	Sequence	IIS-119-878-574-7670	=	1.5×	 	85. Z	7.7	
1640, Ap	eptretipes	IIS-119-924-876-1640	10	5.53	i∡: i,n	85 D	ъу.	
627, App	•	IIS-09-770-696-627	 O	130	بر ار	90 71 (1)	r)	
6120, Ap	Sequence	US-U9-878-574-6120	C	185	3.6	87.4	t)	
3186, Ap	Sequence	US-09-923-876-3186	10	181	3.9	94.2	ι. ω	
7496, Ap	Soquetice	US · U9 · 878 · 574 · 7496	lu	387	س	94. B	t. t.	
28, Appl	eutlet.bes	718-104-444-40XA-2X	Ξ	2/41	4 1	100.2	1	
9047, Ap	Seduction	1.5 th 0.70 th 4.74 /	1.				•	

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: OTHER INFORMATION: PALL
US-09-964-992A-3
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; Patent No. uS20020173633A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 3
LENGTH: 2442
TYPE: DNA
ORGANISM: Lactuca sativa
                                                                                                                                                    Query Match 100.0%, Score 2442,
Best Local Similarity 100.0%, Pred. No. 0;
Matches 2442; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Susiow, Trevor
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Characterization of Phenylalanine Ammonia-Lyase (PAL)
TITLE OF INVENTION: Gene in Wounded Lettuce Tissue
FILE REFERENCE: 023070-124500US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/964,992A CURRENT FILING DATE: 2002-07-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Saltveit, Mikal E.
APPLICANT: Campos, Reinaldo
APPLICANT: No. US20020173633Alogaki, Hiroyuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE: 2000-09-26 NUMBER OF SEQ ID NOS: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/235,956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: lettuce phenylalanine ammonia-lyase (PAL) 1 OTHER INFORMATION: (LSPALL) cDNA
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Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 1812;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local
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CURRENT APPLICATION NUMBER: US/09/964,992A

CURRENT FILING DATE: 2002-07-09

FRIOR APPLICATION NUMBER: US 60/235,956
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APPLICANT: Campos, Reinaldo
APPLICANT: No. US20020173633Alogaki, Hiroyuki
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NUMBER OF SEQ ID NOS: 13
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APPLICANT: The Regents of
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LOCATION: (77)...(2218)
OTHER INFORMATION: PAL2
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                                                                                                                                                                                                                                                                                      AGTITTCTCAGGTGGCGGGGATCGCAGCTGCTAATGACAGTGACACCGTGAAGGTGGAGCT 348
                                                                                                                                                                                                                                                                                                                            GAAGCGGATGGTGGCGGAGTTTAGGAAGCCCGGTGGTGAGATTGGGTGGAGAGACGTTGAC
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                                                                                               TAAGCAAGGCGGTGCTTTACAGAAGGAGCTCATTAGATTTTGAACGCCGGAATATTCGG
                                                                                                                                 TAAAGGAACTGATAGTTATGGTGTCACCACCGGCTTCGGCGCCACCTCTCACCGGAGAAC 468
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85.5%;
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                                                         SEQ ID NO 813
LENGTH: 2154
                                                                                                                                                              APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
APPLICANT: Zhu, Tong
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
TITLE PREPERIOE: SCPIED1300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR FILING DATE: 2001-01-16
PRIOR EPILICATION NUMBER: US 60/264,647
                                                                                                          PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
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ORGANISM: Arabidopsis thaliana
                        TYPE: DNA
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                        1100 GCGGCGCAAAAGGTCCACGAAATGGACCCGTTACAGAAACCAAAACAAGATGGTTATGCT 1159
1000 TTAGCTCAAAAGGTTCACGAGATGGATCCATTGCAGAAACCAAAACAAGATCGTTACGCT 1059
                                                                                                                                                                       1040 GGTCAAATCGAGGCGGCGGCGATCATGGAGTATATTTTGGACGGAAGCGATTACGTCAAG 1099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   560 CATTCAGCCACCAGAGCCGCCATGATCGTCAGAATCAACACCCTCCTCCAGGGTTACTCC
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                                                                                                                940 GGACAAATCGAAGCGGCGGCGATAATGGAGCACATACTCGACGGAAGCTCATACATGAAA
                                                                                                                                                                                                                                 880 GTTATGAGCGGGAAACCTGAGTTTACCGATCATCTGACTCATCGTTTAAAACATCATCCC 939
                                                                                                                                                                                                                                                                                           980 GTTATGCAAGGGAAGCCGGAGTTTACCGATCACTTGACACACAAATTGAAGCATCACCCT 1039
                                                                                                                                                                                                                                                                                                                                                     820 CTATTCGAAGCGAATGTCCAAGCGGTGTTAGCGGAGGTTTTATCAGCGATCTTCGCGGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   760 AAGGAAGGTTTAGCTCTCGTTAATGGCACGGCGGTTGGATCTGGAATGGCGTCGATGGTT 819
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     46 AAAGTGGCGGTTACTACGAAGACTTTGGCAGATCCATTGAATTGGGGTTTAGCAGCGGAT 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGTTTACCCCTCCGTGGAACCATCACCGCCTTCCGGTGACCTTGTCCCATTATCATACATC 739
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                                                                                                                           TTGACTGGAGAAAAGGTTGTGTCTCCGGGAGAGGGAGTTTGATAAGGTCTTCACTGCTATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 49.3%; Score 1203.2; DB 9; Length 2178; Best Local Similarity 73.9%; Pred. No. 4.3e-284; Matches 1542; Conservative 0; Mismatches 538; Indels 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Harper, Jeff APPLICANT: Kreps, Joel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 60/300,111 PRIOR FILING DATE: 2091-06-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 50/264,647
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Wang, Xun APPLICANT: Zhu, Tong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR FILING DATE: 2001-01-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PPIOP APPLICATION NUMBER: HS 60/227,866
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708 OTTOOGGEGACCTIGICCCATIATIATACATCGCCGCCCCTIAACCGGCCGCCCCAACT 767
                                                                                                                                                                       512 TACGAATCAACACTCTCCTCCAA%ATTTTCCGGTATCCGATTTGAGATTCTCGAAGCAA 571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 408 ATAAAGGAACTGATIAGTGTATGGTGTCACCACCGGCTTCGGGGGCACCTCTGACCGGAGAA 467
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APPLICANT: ALBERTE, RANDALL S.
APPLICANT: SMITH, ROBERT
APPLICANT: SMITH, ROBERT
TITLE OF INVENTION: TRANSGENIC PLANTS INCORPORATING TRAIT OF ZOSTEPA MARINA
FILE REFERENCE: PHA-007.01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No. US20020016980A1
                                                                                                                                                                                                                                                                                                                                                                                                            Matches 672;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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TYPE: DNA
ORGANISM: Zostera marina
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                                                                                  157 CAACCCACTCATCGATGTCTCCCGTAACAAGGCTCTCCACGGCGGAAACTTCCAAGGCAC 216
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                   TITLE OF INVENTION:
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Yu, Yang
                                                                                                                                                                                                                         Page, Amy
Matthew, Abraham V
Ledford, Brooke L.
                                       Hurban, Patrick
                                                           Hoffman, Neil
                                                                             Davis, Keith R.
Allen, Keith
                                                                                                                      Slader,
                                                                                                                         Kricker, Maja
Slader, Ted
                                                                                                                                                                  Garcia, Carlos A.
                                                                                                                                                                                    Woessner, Jeffrey P.
Haas, William David
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                                                                                                                                                                                                                                                                                                                                                       Price, Jennifer L.
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; Patent No. US20020102712A1
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CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION TO
                                                                               CURRENT APPLICATION NUMBER: US/09/939,408A CURRENT FILING DATE: 2001-08-24 PRIOR APPLICATION NUMBER: US 09/624,693 PRIOR FILING DATE: 2000-07-24 PRIOR APPLICATION NUMBER: PCT/US01/23270
                                                                                                                                                                                                                                 APPLICANT: Yoshida, Roberta
APPLICANT: Kootstra, Anna
TITLE OF INVENTION: Phenyllalanine Ammonia Lyase Polypeptide and
TITLE OF INVENTION: Polynucleotide Sequences and Methods of obt
TITLE OF INVENTION: Using Same
FILE PEFEPENCE 29479/500NSCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/1
PRIOR FILING DATE: 2000-01-27
SOFTWARE: Patentin Ver.
                         PRIOR FILING DATE: 2001-07-24
NUMBER OF SEQ ID NOS: 30
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TYPE: DNA
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LOCATION: (1)..(2163)
OTHER INFORMATION:
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1380 AATTTTCTGAGCTGGTTAACGAITICTACAACAATGGATTACCATCGAATCTCTCCGGTG 1439
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                                                         1271 CVAACACGATGGAGAAGACTCGCCTCGCVCTCGCCCTGATCGGCAAGCTCAACTTCACGC 1330
                                                                                                         1320 GAGTTTCCATGGACAACACCCGTCTCGCCATTGCTGCAATCGGAAAACTCATGTTCGCTC 1379
                                                                                                                                                                  1211 TCATCGACGTCGAGAACAAGAHGACCCACCACGGCGGCAACTTCCAGGCGDCCGCTGTCG 1270
                                                                                                                                                                                                                      1260 TGATCGACGTTTCCAGAAACAAAGCTTTACACGGTGGTAACTTCCAAGGAACCCCAATCG 1319
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            609 AGGGTTACTCCGGCATCCGATTCGAGATCTTGGAAGCCATCACCAAGTTCCTTAACAACA 668
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 20, Application US/09939408A Patent No. US20020102712A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 09/624,693
PRIOR FILING DATE: 2000-07-24
PRIOR PRIOR PRICATION NUMBER: PTT/US01/23270
PRIOR FILING DATE: 2001-07-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: 29479/500NSCA
CURRENT APPLICATION NUMBER: US/09/939,408A
CURRENT FILING DATE: 2001-08-24
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OTHER INFORMATION: n = A or C or G or T; "n" indicates no consensus at that posit OTHER INFORMATION: near-inpirion of Artificial Sequence: Consensus

OTHER INFORMATION: Sequence of SEQ ID NOS: 12, 16, and 18
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                          669 ACATCACCCCTTGTTTACCCCCTCCGTGGAACCATCACCGCCTCCGGGGGACCTTGTCCCAT 728
                                                                                   557 GCGGCCACTCGGCNGTCCGCCTCGTCGTCCTCCAGGGCGCTCACCAACTTCCTCAACCACG 616
                                                                                                                                         609 AGGGTTACTCCGGCATCCGATTCGAGATCTTGGAAGCCATCACCAAGTTCCTTAACAACA 668
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                                                                                                                                                    TCCGCGCGCGATGGAGTTCGAGTTCAAGAAGCAGTTCGACCCGNTNNTCNCNNCGCTCNTCN 1693
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Paten: No. No. 1988
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Yoshida, Roberta
APPLICANT: Kootstra, Anna
TITLE OF INVENTION: Phenylalanine Ammonia Lyase Polypeptide and
TITLE OF INVENTION. Polypuelectide Sequences and Methods of Obtaining and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/939,408A
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NUMBER OF SEQ ID NOS: 30
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IOCATION: (37)..(2196)
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LOCATION: (494)
OTHER INFORMATION: Other information: y - t or c
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OTHER INFORMATION: Other information:
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Local Similarity 52.2%;
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                                                                                                                                                                                                                                                                                                                                                 Sequence 16, Application US/09939408A Patent No. US20020102712A1
                       SEQ ID NO
                                                                                                   PRIOR APPLICATION NUMBER: US 09/624,693
PRIOR FILING DATE: 2000-07-24
PRIOR APPLICATION NUMBER: PCT/US01/23270
                                                                                                                                                                                                     APPLICANT: Yoshida, Roberta
APPLICANT: Kootstra, Anna
TITLE OF INVENTION: Phenylalanine Ammonia Lyase Polypeptide and
TITLE OF INVENTION: Polynucleotide Sequences and Methods of Obtaining
TITLE OF INVENTION: Using Same
FILE REFERENCE: 29479/500NSCA
                                                             PRIOR FILING DATE: 2001-07-24 NUMBER OF SEQ ID NOS: 30
                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/939,408A
CURRENT FILING DATE: 2001-08-24
                                            SOFTWARE: PatentIn Ver.
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US-09-939-408A-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAGTITCCATGGACAACACCCGTCTCGCCATTGCTGCAATCGGAAAACTCATGTTCGCTC 1379
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; NAME/KEY: CDS]
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US-09-765-873A-31
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PRIOR FILING DATE: 2000-07-27
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846 TOBARTTACAGCORANAAARAARAACTIGTTAACGACACCGCGCGTGBGGTCCGGAAAA 905
                                                                                                     623 AGGGCAAGGAGAAGATCCTGTACGCCCGAGGCGATGGCGCTCTTCTCGAACCTCGAGCCCG 682
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GENERAL INFORMATION:
APPLICANT: Tang, Xiao-Song
TITLE OF INVENTION BIOPRODUTION OF PARA-HYDROXYCINNAMIC ACID
FILE REFERENCE: BC1009 US CIP
FORMERN APPLICATION NUMBER US/09/765,873A
CURRENT FILING DATE: 2001-01-19

PRIOR APPLICATION NUMBER: US 09/627,216
PRIOR FILING DATE: 2000-07-27
PRIOR APPLICATION NUMBER: US 60/147,719

US-09-765-873A-7

; Sequence 7, Application us/09765873A
; Patent No. US20010053847A1

PRIOR FILING DATE: 1999-08-06 NUMBER OF SEQ ID NOS: 38 SOFTWARE: Microsoft Office 97

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; LOCATION: (1)..(2151)
US-09-765-873A-7
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                                                                                                                                           CTCTCATCGACGTCGAGAACAAGACTTCGCACCACGGCGGCAATTTCCAGGCTGCCGCTG 1252
                                                                                                                                                                       CATTGATCGACGTTTCCAGAAACAAACCTTTACACGGTGGTAACTTCCAAGGAACCCCAA 1316
                                               TGGCCAACACCATGGAGAAGACTCGCCTCGGGCTCGCCCAGATCGGCAAGCTCAACTTCA 1312
                                                                                                                                                                                                                                                                                    AAGTAATCCGATCATCAACCAAAATGATCGAGAGGGAAATCAATTCCGTCAACGACAACC 1256
                                                                                            TCGGAGTTTCCATGGACAACACCCGTCTCGCCATTGCTGCAATCGGAAAACTCATGTTCG 1376
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; LOCATION: (1)..(2148)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 9.18;
Best Local Similarity 52.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 603;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/939,408A CURRENT FILING DATE: 2001-08-24 PRIOR APPLICATION NUMBER: US 09/624,693 PRIOR FILING DATE: 2000-07-24 PRIOR APPLICATION NUMBER: PCT/US01/23270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Kootstra, Anna TITLE OF INVENTION: Phenylalanine Ammonia Lyase Polypeptide and TITLE OF INVENTION: Polynucleotide Sequences and Methods of Obtaining and TITLE OF INVENTION: Using Same FILE REFERENCE: 29479/500NSCA
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APPLICANT: Kootstra, Anna
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM. Rhodotorula toruloides
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789 GAGAAGTCCTCAATGCCGAAAAGGCCTTCGCTGC---AGCCGGAGTTGAAGGTCGGCTTCT 845
                                                        653 TCTCCTACATTGCAGCGGCCATCAGCGGTCACCCGGACAGCAAGGTGCACGTCGTCCACG 712
                                                                                                             729 TATCATACATCGCCGGCCTCTTAACCGGCCGCCCCAACTCCAAAGCCGTTGGCCCCACCG 788
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; GENERAL INFORMATION:
; APPLICANT: Tang, Xi
: TITLE OF INVENTION:
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                                                                                                     ; Sequence 9, Application US/09765873A
; Patent No. US20010053847A1
                 TITLE OF INVENTION: GIOPRODUCTION OF FARA-HYDROXYCINNAMIC ACID FILE REFERENCE: BC1009 US CIP
CURRENT APPLICATION NUMBER: US/09/765,873A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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PRIOR APPLICATION NUMBER: US 09/627,216
PRIOR FILING DATE: 2000-07-27
FRIOR APPLICATION NUMBER: US 60/147,719
PRIOR FILING DATE: 1949-08-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Microsoft Office 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(2151)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
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                                                     1193 CTCTCATCHTCATCAAGAACAAGACTTCGGGAACAATTCGGAGGAGATTCGGGTG 1252
                                                                                                                                                                                                                                                                   1317 TCGGAGTTTCCATGGACACACCCGTCTCGCCATTGCTGCAATCGGAAAACTCATGTTCG 1376
                                                                                                                                                                                                                                                                                                                                                                              1013 GAAGCCGCTTTGCTGCCACCATGAGGAAGGTCAAGGTCAAGGACGACGACGACGACGTC 1072
                                                                                                                                                                                                                                                                                                                                                                                                                              1083 GAA---GCGATTACGTCAAGGCGCAAAAGGTCCACGAAATGGACCCGTTACAGAAAAC 1139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1026 - ТБААБСА - - - ТСАСССТББТСАААТТЫЛЫЫ МЕКМЕТКАТСАТЫНЫ АТАТТТЫЛКЫ - 1 082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    953 TCACGCGCCCTCACCCGACGCAGATCGAAGTTGTGGGGAAAGATGCGCAAGCTGCTGGAGG 1012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        533 GCG3CCACTCG3CTGTCCGCCTCGTCGTCCTCGACGACGTCACCAACTTCCTCAACCACG 592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                893 CCATGANGGITCGAAGCGATGGITCGGCGGGTTCGTTCCACCCCTTCACGACG 952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 966 CGATCTTCGCTGAGGTTATGCAAGGGAAGCCGGAGTTTACCGATCACTTGACACACAAAT 1025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    906 TGGCTTCCATGGTTCTATTTGATGCTAATGTACTTGCGTTGTTGTCGGAAGTGTTATCGG 965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               846 TOGAGTTACAGCCGAAAGAAGGCTAGCACTTGTTAACGGCACGGCGCGGGGA 905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     713 AGGGCAAGGAGAAGATCCTGTACGCCCGCGAGGCGATGGCGCTCTTCAACCTCGAGCCCG 772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                        CATTGATCGACGTTTCCAGAAACAAAGCTTTACACGGTGGTAACTTCCAAGGAACCCCAA 1316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACATCACCCCITGTITACCCCTCCGGGGAACCATCACCGCCTCCGGGGACCTIGTCCCAT 728
                                                                                                                                                             ACCITCATIFICACGCCCACGCCCTCCCTCACCATGGAGGGCCGGCCAGITGGACGACGACGACAACC 1192
                                                                                                                                                                                                             AAGTAATCCGATCATCAACCAAAATGATCGAGGGGAAATCAATTCCGTCAACGACAACC 1256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOGTOCTOGGCCGGAAGGAGGGTCTCGGTCTCGTCAACGGCACCGCCGTCTCAGCATCGA 832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAGAAGTCCTCAATGCCGAAAAAGGCCTTCGCTGC---AGCCGGAGTTGAAGGTGCGGTTCT 845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOTOCTACATTGCAGCGGCCATCAGCGGILLACCCGGGACAGCAAGGTGCACGILLGTCCACGI 712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TATCATACATCGCCGGCCTCTTAACCGGCCGCCCAACTCCAAAGCCGTTT4GCCCCACCG 788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCATCACCCCCATCGTCCCCCCTCCGCGGCACCATCTCTGCGTCGGGCGACCTCTCTCCTC 652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGGGTTACTCCGGCATCCGATTCGAGATCTTGGAAGCCATCACCAAGTTCCTTAACAACA 668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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; Sequence 3252, Application US/09878574
; Patent No. US20020110548A1
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LENGTH: 363
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 260; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(15401)B
CURRENT APPLICATION NUMBER: US/09/878,574
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 09/333,535
PRIOR APPLICATION NUMBER: 09/333,535
PRIOR FILING DATE: 1999-06-14
NUMBER OF SEQ ID NOS: 15775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Byrum, Joseph R. APPLICANT: La Rosa, Thomas J. APPLICANT: Thompson, Michael D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OKGANISM: Glycine max
OTHER INFORMATION: Clone ID: LIB3028-013-Q1-B1-G3
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                                                                                                                                                                                                                                                                                                                                                                                                                                        1418 FTACCATCGAATCTCTCCGGTGGACGTAACCCTAGTTTGGACTACGGGTTCAAAGGTGGA 1477
                          1658 CTATGCCAATCCATCGATTTACGCCATTTGGAAGAGAACATGAAATCGACAGTGAAGAAC 1717
                                                                                                                               1598 AGGAAAACCGCAGAAGCAGTCGACATCTTAAAACTCATGTCGTCGACATACTTAGTCGCT 1657
                                                                                                                                                                                                            1538 CATGTTCAAAGCGCCGAACAACAACAATCAAGACGTTAATTCTCTCGGATTAATTTCAGCG 1597
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1617 TCGACATCTTAAAACTCATGTCGTCGACATACTTAGTCGCCTCTATGCCCAATCCATCGATT 1676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1490 TGGCGAACCAGGCGGTCAACTCGCTTGCGCTCATCTCGGCTCGTCGCACGACCGAGTCCA 1549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1557 AACACAATCAAGACGTTAATTCTCTCGGATTAATTTCAGCGAGGAAAAACCGGCAGAAGCAG 1616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1430 ACACCTCGGAGTTGGGACACCTCGCCAACCCTGTGACGACGCATGTCCAGCCGGCTGAGA 1489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1497 ACTISTICTICAGCITTCAGTITTCTCGCAAATCCAGTCACCAACCATCTTCAAAGCGCCGAAC 1556
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1437 GTGGACGTAACCCTAGTTTGGACTACGGGTTCAAAGGTGGAGAAATCGCCATGGCTTCTT 1496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 122 CACGTGCAAAGCGCGGAGCAACACAACCAAGATGTGAACTCTCTGGGGGCTGATTTCATCA 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   y Match 8.1%; Score 198.8; DB 10; Length 363; Local Similarity 71.8%; Pred. No. 7.3e-39;
                                                                                                                                                                                                                                                                                    62 GAAATTGCCATGGCATCTTATTGTTCTGAACTTCAATATTTGGCGGAATCCGGTGACAAGC 121
                                                                                                                                                                                                                                                                                                                                                                                           2 TTGCCTTCAAATCTCACTGCCAGCAGAAACCCCAGCTTGGATTATGGATTCAAGGGAGCT 61
     0; Mismatches 102; Indels
0; Gaps
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Db 242 CTTTGCCAAGCCATTGACTTGAGGCATTTGGAGGAGATTTGAAGAACACGGTCAAGAAC 301

Qy 1718 ACCGTAAGTCGAAGTTGGAAAAAAGGTCCTCACCATGGGGGGTCAACGGTCAACGTTCAACGGTCAACGGTCAACGTTCAACGGTCAACGGTCAACGTTCAACCGTTCAACGGTCAAGTTCAACCGTTCAACCATGGGAGGAGCTTCAACCATGGAGGAGCTTCAACCATGGAGGAGCTTCAACCATGGAGGAGCTTCAACCATGGAGGAGCTTCAACCATGGAGGAGCTTCAACCATGGAGGAGCTTCAACCATGGTTGAATGGAGAGCTTCAACCCT 361

Qy 1778 TC 1779

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Search completed: March 29, 2003, 02:08.56 Job time: 213 secs

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Result
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Maximum Match 1008
Listing first 45 summaries
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4: /cgn2_6/ptudata/1,
5: /cgn2_6/ptudata/1,
6: /cgn2_6/ptudata/1,
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Match Length DB ID
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Sequence 244, App
Sequence 12, Appl
Sequence 12, Appl
Sequence 45, Appl
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Sequence 16, Appl
Sequence 16, Appl
Sequence 18, Appl
Sequence 18, Appl
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Sequence 243, Appl
Sequence 14, Appl
Sequence 15, Appl
Sequence 16, Appl
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Sequence 10, Appl
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Sequence 242, Appl
Sequence 12, Appl
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                                                                      GENERAL INFORMATION:
APPLICANT: Bloksberg, Leonard N. APPLICANT: Havukkala, Ilkka TITLE OF INVENTION: Materials and
                                                                                                                                                                                                                                                                                                                                                                                          1310 ACCCCAATCGGAGTITCCATGGACAACACCCGTCTCGCCATTGCTGCAATCGGAAAAACTC 1369
                                                                                                                                                                                                                                                             1445 ATGTTCGCGCA 1455
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LENGTH: 1520
TYPE: DNA
ORGANISM: Pinus radiata
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                                                          1434 CCGGTGGACGTAACCCTAGTTTGGACTACGGGTTCAAAGGTGGAGAAATCGCCATGGCTT 1493
                                                                                                                                                                                                                                                                                                                                                                                                              1254 ACCCATTGATCGACGTTTCCAGAAACAAGCTTTACACGGTGGTAACTTCCAAGGAACCC 1313
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717 GTGGTGGGCCTAATCCCAGCCTGGATTATGGACTGAAAGGGGCCGAGATCGCTATGGCTT 776
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Local Similarity 67.2%;
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                                                                                                                                                                                                                                  CTATTGGTGTTTCCATGGATAATCTTCGTCTGTCAATTTCAGCAATTGGGAAATTGATGT
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                                                                                                                    TOGOTCAATTCTCAGAGCTTGTGAATGATTACTACAATGGAGGCTTGCCTTCGAATCTGA 716
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                                          : TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-09-615-192A:244
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  Query Match
                                                                                                                                             SOFTWARE. F
                                                                                                                                                                                                                                                              PRIOR FILING DATE: 1997 11 21 PRIOR APPLICATION NUMBER: US OPRIOR FILING DATE: 1996~09-11
                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/615,192A CURRENT FILING DATE: 2000-07-12
                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Materials and Methods for the TITLE OF INVENTION: Modification of Plant Lignin Content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Bloksberg, Leonard N. APPLICANT: Havukkala, Ilkka
                                                                                                                                                                                                              PRIOR APPLICATION NUMBER:
PRIOR FILING DATE: 1998-1
                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 08/475,316
                                                                                                                                                                                          NUMBER OF SEQ ID NOS:
                                                                                                                      LENGTH: 681
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; Sequence 12, Application US/09545686
; Patent No. 6441273
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                                                                                                                    SOFTWARE:
SEQ 1D NO 12
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                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/545,686
CURRENT FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: 60/180,934
PRIOR FILING DATE: 2000-02-08
                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                              FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                  APPLICANT: Gaitan, Alvaro L.
TITLE OF INVENTION: CONSTITUTIVE AND INDUCIBLE PROMOTERS FROM COFFEE PLANTS
                                                                                                                                                               NUMBER OF SEC ID NOS:
                                         ORGANISM. Phenylalanine Ammonia Lyase Consensus Sequence
                                                                     TYPE: DNA
NAME/KEY, unsure
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                                                                                                                                        PatentIn Ver. 2.1
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0; Mismatches 199;
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: OTHER INFORMATION: N at any position in this sequence is either A, C, ; OTHER INFORMATION: G, or T. US-09-545-686-12
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                                                   US-09-615-192A-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 97, Application US/U9615192A Patent No. 6410718
                                                                                                                                           SEQ ID NO 97
  Query Match
                                                                                                                                                                                                                                                                  FILE REFERENCE: 1100.103c4U
CURRENT APPLICATION NUMBER: US/09/515,192A
CUPRENT FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 08/975,316
PRIOR HILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: US 08/713,000
PRIOR FILING DATE: 1996-09-11
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                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US PRIOR FILING DATE: 1998-10-09 NUMBER OF SEQ ID NOS: 405
                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Materials and Methods for the TITLE OF INVENTION: Modification of Plant Lignin Content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
APPLICANT:
                                                                                                                                                                            SOFTWARE:
                                                                          TYPE: DNA ORGANISM: Pinus radiata
                                                                                                                           LENGTH: 577
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                                                                                                                                                                          FastSEQ for Windows Version 3.0
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Pred. No. 5.3e-75;
0; Mismatches 111;
  Score 274.4;
  DB 4;
Length 577
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                      FILING DATE: September 11, 1996
ATTORNEY/AGENT INFORMATION:
NAME: SLEATH, Janet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: BLOKSBERG, Leonard N., HAVUKKALA, Iİkka APPLICANT: and GRIERSON, ALASTALIR W.
TITLE OF INVENTION: MATERIALS AND METHODS FOR TITLE OF INVENTION: THE MODIFICATION OF PLANT LIGNIN CONTENT NUMBER OF SEQUENCES: 88
                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                      SUFTWARE: FASTSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
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                         NAME: SLEATH, Janet REGISTRATION NUMBER:
                                                                                                                                                                                              CLASSIFICATION: 800
                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                  AFPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                            COMPUTER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Law Offices of Ann W. Speckman STREET: 2601 Elliott Avenue, Suite 4185
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REFERENCE/DOCKET NUMBER:
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US-08-975-316-45
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                                                                                                                     CURRENT APPLICATION NUMBER: US/09/615,192A CURRENT FILING DATE: 2000-07-12 PRIOR APPLICATION NUMBER: US 08/975,316 PRIOR FILING DATE: 1997-11-21 PRIOR APPLICATION NUMBER: US 08/713,000
                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Materials and Methods for the TITLE OF INVENTION: Modification of Plant Lignin Content
                                                                                                                                                                                                                                                                                                                              APPLICANT: Bloksberg, Leonard N. APPLICANT: Havukkala, Ilkka
                                                                                                     PRIOR APPLICATION NUMBER - PRIOR FILING DATE: 1996-
                                                                                                                                                                                                                                                           FILE REFERENCE:
                                                  PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 1998-
                             NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO.
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TELEPHONE: 206-269-0565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1265 GACCITTTCCAGAAACAAAGCTTTTACACGGTGGTAACTTCCCAAGGAACCCCCAATCGGAGTT 1324
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LENGTH: 684 base pairs
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APPLICANT: YOShida, Roberta
APPLICANT: YOShida, Roberta
APPLICANT: KOLStra, Anna
TITLE OF INVENTION: Phenylalanine Ammonia Lyase Polypeptide and
TITLE OF INVENTION: Polynacleotide Sequences and Methods of obtaining and
TITLE OF INVENTION: Using Same
FILE REFERENCE: 29479/500NSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-624-693A-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 20, Application US/09624693A
; Patent No. 6355468
                                                                                                                                                                                                                                                                 ; SEQ ID NO 20
Patent No. 6355468
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                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/624,693A CURPENT FILING DATE: 2000-07-24 NUMBER OF SEQ ID NOS: 25
                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Ver. 2.0
  FEATURE: misc_difference NAME/KEY: misc_difference LOCATION: (13, 34, 46, 49, 51, 57, 59, 68, 69, 73, 75 - 77, 79, 82, 84, LOCATION: n = A or C or G or T; "n" indicates no consensus at that posit OTHER INFORMATION: Description of Artificial Sequence: Consensus OTHER INFORMATION: Sequence of SEQ ID NOs: 12, 16, and 18
                                                                                                                                                                                                              LENGTH: 2475
TYPE: DNA
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ORGANISM: Pinus radiata
                                                                                                                                                                                       ORGANISM: Artificial Sequence
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1497 ACTGTTCTGAGCTTCAGGTTTCTCGCAAATCCAGTCACCCAACCATGTTCAAAGCGCCGAAC 1556
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                                                                                                      1394 CTGCCGAGGACCCNTCGCTCTCCTATCACTGCAAGGGCCTCGACATTGCCGCNGCNGCNT 1453
                                                                                                                                                      1437 GTGGACGTAACCCTAGTTTGGACTACGGGTTCAAAGGTGGAGAAATCGCCATGGCTTCTT 1496
                                                                                                                                                                                                            1337 CGCAGCTCACCGAGATGCTCAACGCCGGCCATGAACCGCGGCCTNCCNTCCTGCCT----CG 1393
                                                                                                                                                                                                                                                             1377 CTCAATTTTCTGAGCTGGTTAACGATTTCTACAACAATGGATTACCATCGAATCTCTCCG 1436
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                                                                                                                                                                                                                                                                                                                   TCGCNAACACGATGGAGAAGACTCGCCTCGCNCTCGCCCTGATCGGCAAGCTCAACTTCA 1336
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NUMBER OF SEQ ID NOS: 405
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/615,192A CURRENT FILING DATE: 2000-07-12 PRIOR APPLICATION NUMBER: US 08/975,316 PRIOR FILING DATE: 1997-11-21 PRIOR APPLICATION NUMBER: US 08/713,000 PRIOR FILING DATE: 1996-09-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Bloksberg, Leonard N.
APPLICANT: Havukkala, Ilka
TITLE OF INVENTION: Materials and Methods for the
TITLE OF INVENTION: Modification of Plant Lignin Content
FILE REFERENCE: 11000.1003c4U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US (PRIOR FILING DATE: 1998-10-09
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2120 TIGACCGGAGAAAAGGIGACGICGCCGGGAGAGGAGIITCGACAGGGIGITCACGGCGAIG 2179
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                                                                                                          2060 AAAGCTTGCAGATCGTACCCGTTGTATAGGTTTGTAAGGGAGGAGGTCGGCAGAGGGTTT 2119
                                                                                                                                                                                                                                    2000 GAAGTTGAACGTGTTAGAATCGCTTATGAGAATGATACATTGTCGATTCCAAACAGGATT 2059
                                                                                                                                                                                                                                                                                                                                                     1940 ACCTCCATCTTCCAAAAGATCGCTACCTTCGAAGAAGTATTGAAAGTCCTGTTACCGAAA 1999
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                                                         242 GACGTCGAGGGCGTTCGAGTCCAGTACGAGACAGGCAACCTCGCCATCCCCAACCAGATC 301
                                                                                                                                                                                                                                                                                              182 ACTTCGATCTTCCAAAAGATCGTGGCCTTCGAGGAGGAGCTCAAGGCCCAGTTGCCGAAG 241
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; LOCATION. (37)..(2196)
US-09-624-693A-12
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APPLICANT: Yoshida. Roberta
APPLICANT: Kostira, Anna
APPLICANT: Kostira, Anna
TITLE OF INVENTION. Phenylalanine Ammonia Lyase Polypeptide and
TITLE OF INVENTION. Polynucleotide Sequences and Methods of Obtaining and
TITLE OF INVENTION: Using Same
FILE REFERENCE: 29479/500NSC
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CUPRENT FILING DATE: 2000-07-24
NUMBER OF SEQ ID NOS, 25
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1026 TGAAGCAT---CACCITGGTIAAATCGAGGCGGCGGCGATCATGGA---GTATATTTTGG 1079
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                                              947 CTCTCACGGTGGAGGCCATGGTCGGCCAGCAGGACCTCGTTCGCGCCGTTCATCCACGACG 1006
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           549 ACACACTTICCACATTCAGCCACCAGAGCCGCCATGATCGTCAGAATCAACACCCTCCTCC 608
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                                                                                       CGATICTTCGCTGAGGTTATGCAAGGGAAGCCGGAGTTTACCGATCACTTGACACACAAAT 1025
                                                                                                                                     TGGCTTCCATGGTTCTATTTGATGCTAATGTACTTGCGTTGTTGTCGGGAAGTGTTATCGG 965
                                                                                                                                                                                                                                                                                                                           AGGGAACCGAGAAGATCTTTGCGCGCGAGGCCALCTCGCTCTTTGGTCTCGAGGCAG 826
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Fred. No. 4.3e-52;
0; Mismatches 575; Indels 12; Gaps
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                                                                                                                                                                                                                                                                                      RESULT 11
                                                                                                                                                                                          Sequence 9, Application US/98713000 Patent No. 5850020
                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: HAVUKKAIA, IIKKA
APPLICANT: GELECSON, ADASLAIR
TITLE OF INVENTION: MATERIALS AND METHODS FOR THE
TITLE OF INVENTION: MODIFICATION OF PLANT LIGNIN CONTENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1500 GITCIGAGCITCAGTITCICGCAAATCCAGTCACCAACCAIGTICAAAGCGCCGAACAAC 1559
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1604 ACGTCCTTTCTCCTCCTCCCCCCCCCCCCCGCACCTGCACGCCTCCAGGCCGCTCGACCTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1440 GACGTAACCCTAGTTTGGACTACGGGTTCAAAGGTGGAGAAATCGCCCATGGCTTCTTLACT 1499
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                                                                                                                         Bloksberg, Leonard N.
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COMPUTER READABLE FORM: MEDIUM TYPE: Floppy COMPUTER: IBM PC COM

E: Floppy disk IBM PC compatible

2 I P: COUNTRY:

98121

USA

STATE: STREET:

Seattle WA

2601 Elliott Avenue, Suite 4185

Speckman Picard PLLC

CORRESPONDENCE ADDRESS

ADDRESSEE:

NUMBER OF SEQUENCES:

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US-08-975-316-9
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                                                                                                                                                                                                                                       Sequence 9, Application US/08975316 Patent No. 5952486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: 206-269-0565
TELEFAX: 206-269-0563
INFORMATION FOR SEQ ID NO: 9:
                                                                                                                APPLICANT: BLOKSBERG LEONARD N., HAVUKKALA, IIKKA APPLICANT: and GRIERSON, Alastair W.
TITLE OF INVENTION: MATERIALS AND METHODS FOR TITLE OF INVENTION: THE MODIFICATION OF PLANT LIGN
                                                              NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION NAME: Sleath, Janet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                             1265 GACGTTTCCAGAAACAAAGCTTTACACGGTGGTAAC 1300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1205 CGATCATCAACCAAAATGATCGAGAGGGAAATCAATTCCGTCAACGACAACCCATTGATC 1264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1145 CAAGATCGTTATGCTCCGGTACATCTCCCCCAATGGCTCGGACCTCAAATCGAAGTAATC 1204
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                                                                                                                                                                                                                                                                                                                                                                                589 GATGTCTCCAGGGACATGGCTGTCCACGGCGGCAAC 624
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STREET:
CITY: S
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                                               ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/713,000
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Seattle
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EDNESS: single
                   2601 Elliott Avenue, Suite 4185
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                                            Law Offices of Ann W. Speckman
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                                                                                                                  THE MODIFICATION OF PLANT LIGNIN CONTENT
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Sequence 9, Application US/09211710A; Patent No. 6204434; GENERAL INFORMATION; APPLICANT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-269-0565
                                                                                                                                                                                                       1265 GACGTTTCCAGAAACAAAGCTTTACACGGTGGTAAC 1300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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                                                                                                                                                                 589 GATGTCTCCAGGGACATGGCTGTCCACGGCGCGAAC 624
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SUFTWARE: FastSE
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Local Similarity 69.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
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                                                                                                                                                                                                                                               CGCGCTGCYACTCACTCCATCGAGCGGGAGATCAATTCCGTCAACGACAATCCGTTAATC 588
                                                                                                                                                                                                                                                                                   CGATCATCAACCAAAATGATCGAGAGGGAAATCAATTCCGTCAACGACAACCCATTGATC 1264
                                                                                                                                                                                                                                                                                                                                                                                                          AGCGACTACGTGAAAGAAGCAGCGCGCGTTCACGAGAAAGACCCGTTGAGCAAACCGAAA 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                AGCGATTACGTCAAGGCGGCGCAAAAGGTCCACGAAATGGACCCGTTACAGAAAACCAAAA 1144
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GENERAL INFORMATION:
APPLICANT: Blokebox
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                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 9, Application HS/09615192A Patent No. 6410718
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                                                             CURRENT APPLICATION NUMBER: US/09/615,192A CURRENT FILLING DATE: 2000-07-12 PRIOR APPLICATION NUMBER: US 08/975,316 PRIOR APPLICATION NUMBER: US 08/975,316 PRIOR APPLICATION NUMBER: US 08/713,000 PRIOR FILLING DATE: 1996-09-11 - 1996-09-11 - 1996-09-11 - 1996-09-11 - 1996-09-11 - 1996-09-11 - 1996-09-11 - 1996-10-09
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CURPENT FILING DATE: 1998-12-14
NUMBER OF SEQ ID NOS: 15
                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Materials and Methods for the TITLE OF INVENTION. Modification of Plant Liquin
                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Havukkala, Ilka
APPLICANT: Grierson, Alastair
TITLE OF INVENTION: Materials and Methods for the
TITLE OF INVENTION: Modification of Plant Lignin Content
FILE REFERENCE: 11000.1003c3
SOFTWARE:
                                                                                                                                                                                                                                                                  FILE REFERENCE: 11000 1003c4U
                                        NUMBER OF SEQ ID NOS.
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TYPE DNA
ORGANISM: Pinus radiata
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                    FastSEQ for Windows Version 3.0
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Havukkala, ilkka
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                                                                                                                                                                                                                                              : SEO ID NO 16
: LENGTH: 2787
: TYPE: DNA
: OFGANISM: Fhodotorula mucilaginosa
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; Patent No. 6355468
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                                                                                                                                                            US-U9-624-693A-16
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APPLICANT: Yoshida, Roberta
APPLICANT: Yoshida, Roberta
APPLICANT: KOUStra, Anna
TITLE OF INVENTION: Phenylalanine Ammonia Lyuse Folypeptide and
                                                                     Matches
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                                                                                      Query Match 9.3%;
Best Local Similarity 52.5%;
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                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/624,693A CUPPENT FILING DATE: 2000-07-24
                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Polynucleotide Sequences and Methods of Obtaining and TITLE OF INVENTION: Using Same FILE REFERENCE: 29479/500NSC
                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 25
                                                                                                                                                                           NAME/KEY: CDS
LOCATION: (646)..(2784)
                                                                                                                                                                                                                             FEATURE:
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549 ACACACTRICCACARTCAGCCACCAGCAGCGCGCCARGARGGTCAGAARCAGACACGCCGCCCC 608
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Local Similarity 69.7%;
                                                                     648;
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                                                                 Conservative
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                                                                 0; Mismatches 565;
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                                                                                      Score 228; DB 4; Length 2787; Fred. No. 5.1e-48;
                                                                 Indels 21;
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1136 ACTOGCTTCCGCTCGAAGTCGTCGAAGGGGGATGACCATCCGTGTCACCTCACCTC 1195

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2204 ACGITCICICCICCTCCTCGCCACCIACCICTACTGCGTCCTCCAGGCCGICGACCTCC 1263
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                                                                                             1620 ACATCTTAAAACTCATGTCGTCGACATACTTAGTCGCCTCTATGCCAATCCATCGATTTAC 1679
                                                                                                                                                                                               2144 GCAACCAGGCCATCAACTCGCTCGCCCTCATCTCGGCCGCCGCCGCCGCCGAGGCGAACG
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                                                                                                                                                                                                                                                                                             1560 ACAATCAAGACGTTAATTCTCTCGGATTAATTTCAGCGAGGAAAACCGGCAGAAGCAGTCG 1619
                                                                                                                                                                                                                                                                                                                                                                                                    1440 GACGTAACCCTAGTTTTGGACTACGGGTTTCAAAGGTTGGACAAATTCGCCCATGGCTTTCTTACT 1499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1847 TGATCGACCTCGAGAACAAGATGACCCACCATGGCGAGCCTTCATGGCGAGCAGCGTCG 1906
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Βb

DЬ 204 Вb 9 Ъ Qy Ъ QY Вþ 94 DЬ QY Вb γQ 망 2 DЪ Qy Дb Qy

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UY 1680 GUCATTIGGAA;AAGAACATGAAATCJACAGTJAAGAACACACGITAAGCCAAGICGGGGAAAA 1739
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Search completed: March 28, 2003, 23:41:49 Job time : 119 secs

Qy 1740 AGGTCCTCACCATGGGCGTCAACGGCGAGCTCCA 1773

GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.

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Database
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. Pred. No. is the number of results predicted by chance to have a

SUMMARIES

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Pea PSPAL1 DNA seq	GPAL2 promoter.	Arabidopsis thalia	Pisium sativum L P	Arabidopsis thalia	Arabidopsis thalia	Arabidopsis thalia	CDNA encoding lett	cDNA encoding lett	Description	

Saltveit M,

Campos F, Nonogaki H,

Suslow

(REGC) UNIV CALIFORNIA. 26-SEP-2000; 2000US-235956P

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221.8	223.4	223.4	223.4	223.4	228	235.2	235.2	235.2	244	250	254 2	555	269.4	270.6	272.8	274.4	274.4	274.4	274.4	274.4	282.2	299.4	352	362 6	•	403.2	461.8	549.6	555.4	640	668.8	719	841	84 H 4	3.0.0
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		R. glutinis phenyl	Rhodotorula glutin	Rhodotorula glutin	R. rubra/mucilagin	Finus radiata PAL	Pine phenylalanine	Plant PAL enzyme D	R. graminis PAL po	Furnlyptus grandis	Lolium perenne LpP	Rhodotorula PAL co	Zea mays DNA fragm	Arabidopsis thalia	ddi amatad marlai	Pipus radiata PAL	Pinus radiata phen	Fine phenylalanine	Plant PAL cuzyme D	Pinus radiata PAL	Arabidopsis thalia		Lolium peresne LpP	Euralyptus grandis	perenne	parenne	ddi aunatad mutlon	Fartial 2. marina	Lolium perenne LpP	Pinus radiata PAL	bolium perenne LpP	Eucalyptus grandis	Pisium sativum 1, P	GALP's Promoter.	CHERT ATTITUTE THE CHILD

ALIGNMENTS

RESULT 1 ABK50679

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CDS
                                                                                                                                                                                                                                  ABK50679 standard; cDNA; 2442 BP
                                                            W0200226028-A2
                                                                                                                         Lactuca sativa
                                                                                                                                                Lettuce; phenylalanine ammonia-lyase; plant wounding; plant damage; plant disease; plant browning, vegetable crop; plant; LsPAL1;
                                                                                                                                                                                                                ABK50679;
                         26-SEP-2001; 2001W0-HS30192
                                                                                                                                                                             cDNA encoding lettuce LsPAL1 enzyme
                                                                                                                                                                                             13-AUG-2002 (first entry)
                                                                                             Location/Qualifiers
                                                                            /*tag- a
/product- "LsPAL1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (lactuca sativa) phenylalanine ammonia-lyase (LSPAL) enzymes, and the polynucleotide sequences encoding them. An antibody that binds to a PAL enzyme is useful for measuring the relative amount of PAL levels in a tissue. The polynucleotide sequences encoding PAL are useful in the preparation of plant expression constructs for modifying features of the response of a plant expression constructs for modifying features injury from disease. Disruption or down-regulation of PAL activity can be used to reduce the browning response to wounding in vegetable crops. The present sequence encodes lettuce LSPAL1 enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Fig 5; 46pp, English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel polynucleotide useful in preparing plant expression constructs to modify the response of a plant cell to wounding, damage or other injury from disease causing organisms or from plant pests \,\cdot\,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2442 BP; 693 A; 553 C; 592 G; 604 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-435152/46.
P-PSDB; AAU97130.
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                    661 TAACAACATCACCCCTTGTTTACCCCCTCCGTGGAACCATCACCGCCTCCGGTGACCT 720
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GAGCAATCTGATCAATACCCATTCACGCACAAAGAGTGTGAGTCTAGTGTGAAGAAGAGT 60
                                                               AACAAGCCACACACACTCCACATTCAGCCACACGAGAGCCGCCATGATCGTCAGAATCAACAC 600
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                                                                                                       CCTCCTCCAGGGTTACTCCGGCATCCGATTCGAGATCTTGGAAGCCATCACCAAGTTCCT 660
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel polynoclectide useful in preparing plant expression constructs to modify the response of a plant cell to wounding, damage or other injury from disease causing organisms or from plant pests.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  can be used to reduce the browning response to wounding in vegetable crops. The present sequence encodes lettuce LsPAL2 enzyme.
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                                     709 CTCCGGTGACCTTGTCCCATTATCATACATCGCCGGCCTCTTAACCGGCGGCCGCCCCAACTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                169 GGATOTALI GAACTIGGGGGAGTI GTAGOTGAGGCGTHGACCGGAAGTCACCTTGATGAGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2002-435152/46.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ASTITUTO ASSESSA ASTESSA ASTES
                                                                                                                                                             CACCAAGITCCICAACCACAACGICACCCCITITCICCICICICGCGGGGGACAATTACCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TAAAGGAACGGATAGCTATIGGTGTCACTACCGGGTTCGGAGCTACCTCTCACCGGAGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TAAAGGAACTGATAGTTATGGTGTCAGCAGCGGCTTCGGGGGCCACCTCTCACCGGAGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Campos R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                65.78,
85.58;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1222 CGACAACCGATTGATCGACGTTTCCAGAAAAGACTTTACACGGTGGCAACTTCCAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1069
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                                                                       AGAAGCAGTCGACATCITAAAACTCATGTCGTCGACATACTTAGTCGTCATGCCAATC 1658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AATGTTCGCTCAGTTCTCTGAGCTTGTCAACGATTTTTACAACAACAACGGCTTGCCATCCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AACCCCAATCGGAGTTTCCATGGACAACACCCGTCTCGCCATTGCTGCAATCGGAAAACT 1368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CGACAACCCATTGATCGACGTTTCCAGAAACAAAGTTTACAGGGTGGTGGTAGTACTTCCAAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAAAGCCCTTGGCCCCACCGGAGAAGTCCTCAATGCCGAAAAGGCCTTCGCTGCAGCCGG
TTGCAGCGCACATACCCATTAATGCAGAAGCTCCGACAGGTTCTGGTGGACGACGCTCT
                                                                                                                                           CGAGAAAGATCTCCTCCGTGTTGTTGATCGTGAATACGTCTTCGCTTACATCGACGACGACGT 1848
                                                                                                                                                                                                                                                                                           AGTCGCGAAAAAGGTCCTCACCATGGGCGTCAACGGCGAAGCTCCACCCGTCGAGATTCTG
                                                                                                                                                                                                                                                                                                                                                                   CATCGACTTGAGGCATTTGGAAGAGAACCTGAAATCCACAGTGAAGAACACAGTGAGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                       CATCGATTTACGCCATTTGGAAGAGAACATGAAATCGACAGTGAAGAAGAGAGGGTAAGCCA 1728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CGCCGAACAACACAATCAAGACGTTAATTCTCTCGGATTAATTTCAGCGAGGAAAAACCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCTCTCCGGCGGCCGGAATCCAAGTTTGGATTACGGGTTCAAAGGTGCAGAAATCGCCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCTCTCCGGTGGACGTAACCCTAGTTTGGACTACGGGTTCAAAGGTGGAGAAATCGCCAT 1488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCAMATCGAAGTAATCCGATCATCAACCAAAATGATCGAGAGGGAAATCAATTCCGTCAA 1248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTTACAGAAACCAAAACAAGATCGTTATGCTCTCCGTACATCTCCCCAATGGCTCGGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTTACAGAAACCAAAACAAGATCGTTATGCTCTCCGTACATCTCCCCAATGGCTCGGACC 1188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTATATTTTGGACGGAAGCGATTACGTCAAGGCGCGCAAAAGGTCCACGAAATGGACCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CGCCGTGGGATCCGGGATGGCGTCGATGGTGCTATTTGATGCTAATGTTCTTGCATTGTT
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                                                                                                                                                                                                                   CGTCGCGAAGAAGATCCTAACCACCGGCGTCAATGGCGAGCTCCACCCTTCTCGCTTCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGAATCAGTCGAGATCTTAAAACTCATGTCAACCACACATACTTAGTAGCTCTATGTCAATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGCTTCTTACTGTTGTGAGCTCCAGTTTCTCGCCAATCCAGTCACMACCACGTTCAMAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AACCCCAATCGGAGTTTCCATGGATAACACACGTTTGGCGATCGCCGATCGCCAICGGAAAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCACTTAACACACAAATTGAAGCATCACCCCGGTCAAATCGAGGCGGCGGCGATCATGGA 1041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGTTGAAGGTGGTTTCTTCGAGTTACAGCCGAAAGAAGGCCTAGCACTTGTCAACGGCAC
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                       25-FEB 1999
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           04-MAY-1999,
                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                       Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway;
                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana DNA fragment SEQ ID NO: 68947.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1909
                                                                                                                                                                                                                                                                                                                                                                         metabolic pathway; promoter; termination sequence;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-0CT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2233 AATACTTTTTATGAGTTTTG 2252
                                                                                                                                                                                                                                                                  25-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGAGTGTGTTCAAGGGTGGAATGGTGTTCCTCTCCGATTTCATAGTTATTTTGTTCATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGAGGAGTTCGACAGGGTGTTCACGGCGATGTGCAAAGGTCAAATTATTGATCCGTTGTT 2208
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                     990S-0130449.
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990S-0132048.
990S-0132407.
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99US-0130077.
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           99US-0132484
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920 CTATTTGATGCTAATGTACTTGCGTTGTTGTCGGAAGTGTTATCGGCGATCTTCGCTGAG 979
                                       862 AAGGAAGGTTTAGCTCTCGTTAATGGCACGGCGGTTGGATCTGGAATGGCGTCGATGGTT 921
                                                          860 AAAGAAGGCTAGCACTTGTTAACCGCACCGCGGTGGGGTCCGGGATGGCTTCCATGGTT 919
                                                                                                                                                                                      742 CCCGGACTTCTCACCGGCCGTCCTAATTCCAAAGCCACCGGTCCCGACGGTGAATCGCTA 801
                                                                                                                                                                                                                                                                                       680 TGTTTACCCCTCCGTGGAACCATCACCGCCTCCGGTGACCTTGTCCCATTATCATACATC 739
                                                                                                                                                                                                                                                                                                                                                                               620 GGCATCCGATTCGAGATCTTGGAAGCCATCACCAAGTTCCTTAACAACAACATCACCCCT 679
                                                                                                                                                                                                                                                                                                                                                                                                                   562 CAATCCGCCACAAGAGCCGCCATGCTCGTCAGAGTCAACACTCTTCTCCAAGGATACTCC 621
                                                                                                                                                                                                                                                                                                                                                                                                                                        560 CATTCAGCCAGAGAGCGCCATGATGATCGTCAGAATCAACACCCTCCTCCAGGGTTACTCC 619
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              148 AAAGTGGCGGTTACTACGAAGACTTTGGCAGATCCATTGAATTGGGGTTTAGCAGCGGAT 207
                                                                                                                802 ACCGCGAAAGAAGCTTTTGAGAAAGCCGGAATCAGTACTGGATTCTTCGATTTACAACCT 861
                                                                                                                                                   800 AATGCCGAAAAGGCCTTCGCTGCAGCCGGAGTTGAAGGTGGGTTCTTCGAGTTACAGCCG 859
                                                                                                                                                                                                                                740 GCCGGCCTCTTAACCGGCCGCCCAACTCCAAAGCGTTGGCCCCCACCGGAGAGACTCCTC 799
                                                                                                                                                                                                                                                                 622 GGATUCGATTUGAGATUUTUGAAGUGATTACAAGTUTCCTCAACCACAACATUTCTCCG 681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           502 ATTAGATTTTTGAACGCCGGAATATTCGGAAACACGAAGGAGACATGTCACACACTGCCG 561
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RESULT 4 ACC45027 ACC45027 XX ACC AAC45027; XX ACC AAC45027; XX ACC AAC45027; XX ACC AAC45027; XX ACC ACC5027; XX ACC5027;	Db 2002 GAAGTTGAAGCGTAGAACTGTTGTATGAACTGGGAAGCGTTTCTTTTTTTT
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                1066 ASTATATITIGGAOSSAAGOSATTAOSTOAASSOGGOGOAAAASSTOOAOSAAATSSAOO
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                                                 ATCATCTCACTCACAGACTTAAACATCATCCCGGTCAAATCGAAGCGGCGGCGATAATGG
                                                                               ATCACTTGA/ ACACAAATTGAA//CATCACCCTG/GTCAAATC/AA/GG/CA/GG/GA/GATCAT/GG
                                                                                                                                                                              CGGCGGTTGGATCTGGAATGGCGTCAATGGTGTTATTCGAAACGAATGTTCTCTCTGTTT
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GAGAGGAGTTCGACAGGGTGTTCACGGCGATGTTGCAAAAGGTCAAATTATTGATCCGTTGT 2207
                                                                                                                                           | GGTTTGTAAGGGAGGAGTTTGGAGAGAGTTTTT-GACCCGAGAAAAGGTGACGTCGCCGG-2147
                                                                                                                                                                                                                    ATTAACCGGAACATTCGGCTATTCCCGGAACAGGATTCAAGGAATTGTAGGTCGTATTCCATTTGTATA 2011
                                                                                                                                                                                                                                                    AGAATGATACATTGTCGATTCCAAACAGGATTAAAAGCTTGCAGATGGTACCGGTTGTATA
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                                        2300 TITTTTTTTTTTTTT 2316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1640 TCGACATACTTAGTCGCTCTAIGCCAAICCAICGAIITACGCCATTTGGAAGAGAGAACATG 1699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1523 GCTIAATICCAGTCACAAGCTATGTTCAATCAGCTGAGCAACATAATCAAGATGTGAACTICT
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2303 AATTITAATTITGCTGT 2319
                                                                                 2243 ATTICCGATTTGCTAAGAGAGCATTCCTCTGTTTCTGTTTCTGTGTFTFTGTGTFTTTGTGTTTTCT2302
                                                                                                                          2240 CTTCCAATATGITAGGAAAGTGAGTGAAACGGTTTGAACTGTAITAITATATATATTCTGT 2299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1883 CTGAGACAAGTTATTGTTGATCACGCTTTGTCTAACGGTGAGACTGAGAAGAATGCAGTG 1942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1643 АСААСАТТССТТЭТТЭЭЭАТАТЭГЭААЭГТЭТТЭАТТТЭАЭЛЭЭЛЭГЭЭЭЭЭЭЛЭЭЛЭЭДТЭТЭ 1702
                                                                                                                                                                                                                                                    AAGGAATGTAGGTCGTATCCGTTGTATAGGTTTTGTGAGGGAAGAGGTTGGAACGAAGTTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACCTCCATCTTCCAAAAGATCGCTACCTTCGAAAGAAGAATTGAAAGTCCTGTTTACCGAAA 1999
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                                                                                                                                                                     TGTGAAGGTAAACITATTGAFCGTTGATGGATGGATGTCTCAAGGAATAGAACGGAAGCTCCC 2242
                                                                                                                                                                                           TGCAAACGTCAAATTATTCATCCGTTGTTTGGAGGTTGTTGGAGGGTTGGAATGGGGAACCT 2239
                                                                                                                                                                                                                                                                                                                                                                                       AAAGCTTGCAGATCGTACCCGTTGTATAGGTTTGTAAGGGAGGAGCTCGGCAGAGGGTTT 2119
                                                                                                                                                                                                                                                                                                                                                                                                                             GAAGTTGAAGCGCTAGAGCAGCTTATGGGACTGGAACTGCGACTGCTAACCGGATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACTTCGATCTTTCAAAAGATTGGAGCTTTTGAAGAGAGGAAGAGTTAAGGGTGTGCCAAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTCGGATTAATITCAGCGAGGAAAACCGCAGAAGCAGTCGACCATCTTAAAACTCATGTCG 1639
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The sequence is that of the phenylalanine ammonia lyase (PAL) gene from Pisum sativum L. The gene may be used to produce PAL recombinantly. Plants contg. the PAL gene can contain a large amt. of phenyl propanoid isoflavonoid. See also AAQ33019.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2607 BP; 795 A; 485 C, 577 G, 750 T; 0 other;
                          530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 7; 9pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New phenylalanine ammonia lyase gene from Pisum sativum L plasmid contg. gene, and E. coli transformed with plasmid, for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               prepn. of lyase.
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                                                                                                                                                                   555 TCAGAATCTGCTAGGGCTGGCGTTAAGGCGAGCAGTGACTGGGTGATGGAGAGTATGAAC
                                                                                                                                                                                                                                                                                        441 AAGCGTATGGTGGAGGAGTACAGGAAGCCGGTGGTCCGCCTTGGTGGCGAGACACTGACG 500
                                                                                                                                                                                                                                                                                                                                                                              170 GATICCATTGAACTGGGGAGTTGCAGCGGAGGCGTTGACCGGAAGTCACCTTGATGAGGTG 229
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                                                                                                                                                                                                                                                          290 GTTTCTCAGGTGGCGGGATCGCAGCTGCTAATGACAGTGACAGCGTGAAAUUTGGAGCTG 349
                                                                                                                                                                                                                                                                                                           230 AAGAAGATGGTTGCGGAGTTCAGAAAGCCGGTGGTGAAGCTCGGAGGAGAGACGCTTACA 289
                                                                                                                                                                                                                                                                                                                                                 381 GATCCTTTGAATTGGGGTGTTGCCGCCGAGGCAATGAAAGGGAGTCACTTGGATGAGGTG 440
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               AATGGAACGGAAACAAGCCACACTTCCACATTCAGCCACCAGAGCCGCCATGATCGTC 589
                                             AAACAAGGTGGTGTTTTGCAGAAAGAACTCATCAGGTTTTTTGAATGCTGGAATATTTTGGA 734
                                                                                                                                                                                                                               ATTTCTCAGGTGGCTGCCATTGCCGCACATGATCATGGT-----GTTAAGGTGGAGTTG
                                                                          AAGCAAGGCGGTGCTTTACAGAAGGAGCTCATTAGATTTTTGAACGCCGGAATATTCGGC
                                                                                                       AAAGGCACAGACAGTTACGGTGTTACTACCGGTTTCGGCGCCACCTCTCACCGGAGAACC 674
                                                                                                                                     AAAGGAACTGATAGTTATGGTGTCACCACCGGCTTCGGCGCCACCTCTCACCGGGGAACT 469
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Location/Qualifiers 126..2456
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1812 TATGAAGCCATTGAGATCCTTCAACTCATGTCTTCCACATTCTTGATTGCACTTTGCCAA 1871
                      1607 GCAGAAGCAGTCGACATCTTAAAACTCATGTCGTCGACATACTTAGTCGCTCTATGCCAA 1666
                                                                                                                             1550 GCCG---AACAACACAATCAAGACGTTAATTCTCTCGGATTAATTTCAGCGAGGAAAACC 1606
                                                                                                                                                                       1692 GCTTCTTATTGTTCTGACTTACAATATCTTGCAAACCCAGTTACAACTCATGTTCAAAGT 1751
                                                                                                                                                                                                                                                          1632 CTCTCAGCTAGTAGAAATCCCAGCTTGGATTATGGATTCAAGGGATCCGAAATTGCCATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1392 CTTATTGAAGTCATTAGATTCTCTACTAAGTCAATTGAGAGGGAGATCAACTCTGTTAAT 1451
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                590 AGAATCAACACCCTCCTCCAGGGTTACTCCGGCATCCGATTCCAGATCTTGGAAGCCATC 649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           735 AATGGAACTGAGTCAAGCCATACACTACCACACACAGCAACAAGAGCTGCCATGCTTGTG 794
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                                                                                  GCTGAGCAACAACAACCAAGATGTGAACTCTTTGGGTTTGATATCTTCTAGGAAAACA 1811
                                                                                                                                                                                                                CTCTCCGGTGGACGTAACCCTAGTTTGGACTACGGGTTCAAAGGTGGAGAAATCGCCATG
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                                                                                                                   AGCGCAGAGCATAACCÁÁGACGTTAATTTCCCTAGGGCTAATCTCTAGCAGGAAAACT
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control of a promoter, using Agrobacter tumefacters (pref. LB4404) as a vector. Sequence inhibits lighth biosynthesis in the plant improving digestibility of animal foder, and useful in production of paper pulp etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1837
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1657 A 'ARACRICATETC' TO CAARTERITERAC EGAGAGIACOCTGTTCT CATACGCAGACGAT 1716
                                                                   Antisense CAD gene fragment is inserted into the plant under the
                                                                                                      Disclosure; Fig 6; 42pp; English
                                                                                                                                     Recombinant DNA, for plants with reduced lignin content - for improved animal fodder and paper pulp prodn.
                                                                                                                                                                                            WP1: 1990-261294/35
                                                                                                                                                                                                                            Schuch WW,
                                                                                                                                                                                                                                                                                                15-DEC-1988;
                                                                                                                                                                                                                                                                                                                                 14-DEC-1989;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     SR1; Agrobacterium tumefaciens; lignin; ds;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAQ05768 standard; DNA; 5291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2147 GGAGAGGAGTTOGAGAGGGTGTTGAGGGTGATGTGCAAAGGTGAAATTALTGATGGTTG 2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1957 COGITTGTCCGCCATGAGCTAAATACTGAACTGCTTACTGGAGAGAATGTTCGGTCGCCA 2016
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1847 GIFFGCAGCGGCACATACCCAFFAA DCCAGAAGCTCCGGACAGGFFCTGGTCGGACCACGCC
                                                                                                                                                                                                                                                             (SCHU/) SCHUCH W W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLAANCARCGGCGAAACGGAAGAAGAAGAACAACACCTCCATCTTCCAAAAGAALCGCIACC
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                                                                                                                                                                                                                           Knight ME,
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1461 ACGGGTTCAAAGGTGGAAANCGCCATGGCTTCTTACTGTTCTGAGGTTCAGTTTCTCC 1520
                                                                                                                                                                                                           4156 AGGCCTTGCATGGTGACTTCCAAGGAACTCCAATTGGAGTCTCCATGGATAACACCC
                                                                                                                                                                                                                               1281 AAGCTTTACACGGTGGTAACTTTCCAAGGAACCCCAATCGGAGTTTCCATGGACACACCC 1340
                                                                                                                                                                                                                                                                                   4096 CAATTGAGAGGGAGATCAACTCAGTCAATGACAACCCTTTGATTAGTGTGTCTAGGAACA 4155
                                                                                                                                                                                                                                                                                                                      1221 TGATCGAGAGGGAAATCAATTCCGTCAACGACAACCCATTGATCGACGTTTCCAGAAACA 1280
                                                                                                                                                                                                                                                                                                                                                                                  1161 TCCGTACAICICCCCAATGGCTCGGACCTCAAATCGAAGTAATCCGATCATCAACCAAAA 1220
                                                                                                                                                                                                                                                                                                                                                                                                                                       3976 CTGCTAAGAAGTTGCATGAGATAGATCCTTTGCAGAAACCCAAACAAGATCGCTATGCCC 4035
                                                                                                                                                                                                                                                                                                                                                                                                                                                         1101 CGGCGCAAAAGGTCCACGAAATGGACCGGTTACAGAAACCAAAACAAGATCGTTATGCTC 1160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 5291 BP; 1512 A; 1061 C; 971 G; 1747 T; U other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    501 TTAGATTTTTGAACGCCGGAATATTCGGCAATGGAACGGAAACCAACACCACCACCTTCCAC 560
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                                                                                                                                                    GTCTCGCCATTGCTGCAATCGGAAAACTCATGTTCGCTCAATTTTCTGAGCTGGTTAACG 1400
                                                       ACTATTACAATAATGGGTTGCCTTCTAATCTCACTGCCAGCAGAAACCCCCAGCTTGGATT 4335
                                                                                           ATTTCTACAACAATGGATTACCATCGAATCTCTCCGGTGGACGTAACCCTAGTTTGGACT 1460
                                                                                                                                GTTTGGCTÄTTGCTTCAÄTTGGAÄÄACTCÄTGTTTGCTCAATTCTCTGATCTTGTCAATG 4275
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                                                      TTCCAATTTGTTAG 5129
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AAC61194
                                   12-FEB-2001 (first entry)
                                                 AAC61194 standard; DNA; 4415 BP
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Pea; promoter; plant; prevention; pathogen; infection; ds

Pea PSPAL1 DNA sequence SEQ ID 9.

Pisum sativum

JP2000245463-A

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This invention relates to hove! DNA with promoter activity, comprising the promoter fragments represented by AACE1186 and AACE1187. The DNA can be used for the prevention of inferritor of a pathograph microbe in the roots, leaves and stems of a plant. The present sequence represents the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4415 BP; 1415 A; 724 C, 794 G, 1482 T; 0 other,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pea PSPALL gene used in an example to illustrate the use of the promoter of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure, Page 11:13, 17pp, Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel DNA with promoter activity, useful for the prevention of a pathogenic microbe from the roots, leaves and stems of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WP1; 2000-675181/66
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(NISB ) JAPAN TOBACCO INC.
(TAKS ) TAKASAGO PERFUMERY CO LTD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26 FER 1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2542 ACACAGCAACAAGAGCTGCCATGCTTGTGAGAATCAACACTTCTCCAAGGTTATTCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            y Match 39.8%; Score 972.4; DB 21; Length 4415; Local Similarity 70.1%, Fred. No. 4.8c-165;
                                                                                                                                                                                                                                                                                                                                                             AAGAA&&&TA&AATTIGTTAAYAAACCOO'YSTGG&STCCG&GATGGTTCCATGGTTC 920
                                          CGGCGCAAAAGGTCCACGAAATGGACCCGTTACAGAAACCAAAACAAGATCGTTATGCTC 1160
                                                                                                         CTGGTTTACTAACGGGAAAGCAAATTCAAAAGCTCATGGGAACCTCTGGGGGAAATTCTTA 2778
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                                                                                  GTCANATTGAGGCTGCTATTATGGANCACATTTTGGATGGAAGTGCTTATGTCAAAG
                                                                                                                                                                     TTATGCAAGGGAAACCTGAGTTTACTGATCATTTGACACATAAATTGAAGCACCATCCTG
                                                                                                                                                                                                                                                        TATTTGAAGCTAACATATTGGCTGTCTTGTCTGAAGTCCTATCCGCTATTTTTGCTGAAG 2958
                                                                                                                                                                                                                                                                                              TATTTIGATICCTAATTITACTTIGCGTTGTTGTGTGGGAAGTGTTATCGGCGATCTTCGCTGAGG 980
                                                                                                                                                                                                                                                                                                                                        AAGAAGGTCTTG: ACTTGTTAATGGAACTGCTGTTGGTTCTGGTTTAGCTTCTATTGTTC 2898
                                                                                                                                                                                                                                                                                                                                                                                                                           ATGCAAAAGAAGCTTTTCAGTCAGCTGAAATCAATGATGGTTTTCTTTGAATTGCAACCAA 2838
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                                              4159 GTCAAGGAAAGATCATCGATCCTTCTTCTTCAATGCTTGGGAAGACTGGAACGGTGCTCCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 39.8%; Score 970.8; DB 14; Length 4415; Hest Local Similarity 70.0%; Pred. No. 9.4e-165; Matches 1335; Conservative 0; Mismatches 567; Indels 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2482 TCAGGTTTTGAATGCTGGAATATTTGGAAATGGAACTGAGTCAAGCCATACACTACCAC 2541
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             capable of artificially accelerating or suppressing the transcription of the structural gene of a plant.
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2719 CIGGTTTACTAACGGGAAGACCAAAIICAAAAGCTCATGGGACCTCTGGGGAAATTCTTA 2778
                                                                                                                        2602 GAATTAGATTTGAAATCTTGGAAGCTATAACCAAACTCATTAACAACAACGTCACCCCAT 2661
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The regulatory fragment of the phenyl alanine ammonia lyase gene is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 2; Page 7-8; 9pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Regulator gene of specified sequence - and phenylalanine ammonia lyase gene of pea with specified sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1993-231495/29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Phenylalanine ammonia lyase gene with 5' regulatory gene
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                                                                                                                                                                      681 GITTACCCCTCCGTGGAACCATCACCGCCCGGTGACCTTGTCCCATTATCATACATCG 740
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                       Antisense CAD gene fragment is inserted into the plant under the control of a promoter, using Agrobacter tumefacters (pref LB4404) as a vector. Sequence inhibits lighin biosynthesis in the plant improving digestibility of animal inder, and useful in production
                                                                                                                                                                                                                                                                                                                                                             CA2005597 - A
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                                                                                                   Disclosure; Fig 7; 42pp; English.
                                                                                                                                improved animal todder and paper pulp prodn
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                                                                                                                                                                                                          Schuch WW, Knight ME,
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                             Pisum sativum
                                                                                                                                          Pisium sativum L PAL gene
                                                                                                                                                                                        07-MAY-1993 (first entry)
                                                                                                                                                                                                                                                                                  AAQ33019 standard; cDNA; 1707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2178 TGTGCAAAGGTCAAATTATTGATCCGTTGTTGGAGTGTCTTGGAGGGTGGAATGGGGAAC
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                                                                                            Phenylalanine ammonia lyase; phenyl propanoid isoflavonoid; plant;
                                                                                                                                                                                                                                      AAQ33019;
                                                                                                                                                                                                                                                                                                                                                                                                                                             2298 GTTTTTTTTTTTTTTTTTTAAATTTTATTTGCAT 2331
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2726 TGCTCACCGGCGAAAAAGCTCTCTCTCCAGATGAGGAATTTGAAAAGGTTTATACAGCCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1758 TCAACGCCGACCTCCACCCGTCGAGATTCTGCGAGAAAGATCTCCTCCGTGTTGTTGATC 1817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1578 CTCTCGGATTAATTTCAGCGAGGAAAACCGCAGAAGCAGTCGACATCTTAAAACTCATGT 1637
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2786 TGTGTCAAGCAAAGATAATTGATCCAATTCTGGAATGTCTAGAAGATTGGAACGGGGTTC
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                                      1336 CACCCGTCTCGCCATTGCTGCAATCGGAAAACTCATGTTCGCTCAATTTTCTGAGCTGGT 1395
                                                                                                             1276 AAACAAAGCTTTTACACGGTGGTAACTTCCAAGGAACCCCAATCGGAGTTTCCATGGACAA 1335
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The sequence is that of the phenylalanine ammonia lyase (PAL) gene from Pisum sativum L. The gene may be used to produce PAL recombinantly. Plants contg. the PAL gene can contain a large amt. of phenyl propanoid isoflavonoid.
                                                                                                                                                                                                                                                                                                                                                                                             1096 CAAGGCGGCGAAAAGGTCCACGAAATGGACCCGTTACAGAAACCAAAACCAGATCGTTA 1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1707 BP; 496 A; 345 C; 377 G; 489 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 8; 9pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New phenylalanine ammonia lyase gene from Pisum sativum L. - plasmid contg. gene, and E. coli transformed with plasmid, for
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CACTCGTTTGGCTCTTGCATCTATCGGCAAACTCATGTTTGCTCAATTCTCCGAGCTTGT
                                                                                         GAACAAGGCATTGCATGGTGATTTCCAAGGAACCCCAATTGGAGTCTCCATGGACAA
                                                                                                                                                                                                              CAAAATGATGGAGAGGGAAATGAATTGGGTGAAGGAGAAGGCATTGATGGAGGTTTGGAG 1275
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Plant; lignin; lignin biosynthetic pathway; Eucalyptus grandis;
                                                                                                                                                                                       AAA68152 standard; DNA; 1455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1081 CAGGGAGTATGTATTTTCCTACATAGATGACCCATACAGTGGTACATACCCACTGATGCA 1140
                                              Eucalyptus grandis PAL nucleotide sequence SEQ ID NO:245
                                                                                                                                              AAA68152;
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                                                                                                                                                                                                                                                                                                                            ACCTCTTCCAATATGTT 2252
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                                                                                                                                                                                                                                                                                                                                                                                                                                             GATIGTICCAAAGGTICAAATTILATTIIGATICCGTTIGTIILIGGAGTIGTTIILIGGAGGGTTGCAATIGGGGA 2235
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polynucleotides can be used for modulating lighin content, lighin composition and the structure of a plant, especially eucalyptus and pine species, and for modifying the activity of an enzyme involved in lighin biosynthetic pathway, and for producing a plant having altered lighin content, composition and structure. They can be used for designing probes and primers useful for detecting similar DNA and RNA sequences in any
                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes isolated polynucleotides and proteins encoding and representing the enzymes cinnamate 4-hydroxylase (C4H), coumarate 3-hydroxylase (C3H), phenolase (PNL), O-methyl transferase (OMT), cinnamyl alcohol dehydrogenase (CAD), cinnamyl-CoA reductase (CCR), phenylalanine ammonia-lyase (PAL), 4-coumarate:CoA ligase (4CL), coniferol glucosyl transferase (CGT), coniferin beta-glucosidase (CBG),
                                                                organism and for PCR amplification. The limin content can be efficiently modified using the polynucleotides. AAAb7908 to AAAb8201 and AAB16341 to AAB16449 represent polynucleotide and protein sequences used in the
                                                                                                                                                                                                                                                                                coumerate CoA ligase, cytochrome P450 LXXIA, diphenol oxidase, flavanol glucosyl transferase, flavenoid hydroxylase, and isoflavone reductase, which are involved in the lignin biosynthetic pathway. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel polynuclectide encoding enzymes involved in lignin-biosynthetic pathway useful for producing transgenic plants especially eucalyptus and pine species having altered lignin content, composition and
Sequence 1455 BP; 307 A; 442 C, 431 G, 275 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                     laccase, peroxidase, ferulate-5-hydroxylase (F5H), alpha amylase, caffeic acid methyl transferase, caffeoyl CoA methyl transferase,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 131-132, 213pp, English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-OCT-1998;
14-JUL-1999;
                                          exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-OCT-1999;
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Query Match y Match 29.4%; Score 719; DB 21 Local Similarity 75.3%; Pred No le-119; Conservative 0 Mismatches 290, DB 21; Indeis

Ş 밁 Db Š Бþ VΥ J. Matches 410 AAAGGAACTGATAGTTATGGTGTCACCACCGGCTTTCGGCGCGCCACCTCTCACCGGAGAACT 469 4.25 TCGGAGGCGGCCGTCCCAGGGTCAAGGCCAGCAGCAGCTGGGTCATGGAGAGCATGAAC 170 GATECATTGAACTGGGGAGTTGCAGCGGAGGCGTTGACCGGAAGTCACCTTGATGAGGTG 374 ATAGCCCAGGTGGCGGGGGGTGGCGAGT------CAGGAGGGGGTAGGGGTTGGAGCTC 290 ATTTCT/AMATAMACAMATCACAGCTACTAATAACAGTGACACCACCATAAAAAGATAAAAGACTAAAA 230 AAGAAGATGGTTGCGGAGTTTCAGAAAGCCGGTTGGTGAAGCTTCGGAGGAGAGAGGCTTTACA 289 350 TCGGAAGCCGCGAGGGCTGGAGTTAAGGCGAGTAGTGATTGGGTTATGGAGAGGATGAAT 254 GARCCACTGAACTGGGGGGGGGGGGARCAGCAGCCCTCACAGGGAGCCACCTCGACGAGGTG 313 Ġ

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                                                                                                                                                                                                                                                                                              ACCCCGATTGGTGTCTCCATGGACAACACTCGCCTGGCGGTTGCGTCCATAGGGAAGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCGGAAGTGTTATCGGCGATCTTCGCTGAGGTTATGCAAGGGAAGCCGGAGTTTACCGAT 1009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCAAGTTCCTCAACCACAACATCACCCCGTGCCTGCCCTCAGGGGCACCATCACTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1204
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Matches Query Match

Similarity

27.4%; Score 668.8; DB 24 65.8%; Pred. No. 9.8e-111;

DB 24; 475;

Length 1503;

Conservative

16;

Mismatches

Indels

0,

0,

65

897 GGTCCGGGATGGCTTCCATGGTTCTATTTGATGCTAATGTACTTGCGTTGTTGTCGGAAG

957 TGTTATCGGCGATCTTCGCTGAGGTTATGCAAGGGAAGCCGGAGTTTACCGATCACTTGA 1016 6 GGCTCCGGCTCGCGTCCATGGTGCTCTTCGAGGCCAACATCCTTAGCCTCCTTGCCGAGG

Sequence 1503 BP; 339 A; 427 C; 407 G; 310 T; 20 other;

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hybridisation probes to screen libraries from the desired plant. Short segments of (I) or its fragment are useful in amplification protocols to amplify longer nucleic acids or its fragments encoding homologous genes from DNA or RNA. (I) or its fragments are useful as molecular genetic markers for quantitative trait loci (QTL) tagging, QTL mapping, DNA fingerprinting, and in marker assisted selection, particularly in ryegrass and fescues, and in forage and turf grass improvement, e.g. tagging QTLs for herbage quality traits, dry matter digestibility,
                                                                                                                                                                                                                                                                                                                                                      ryegrass (Lolium perenne) or fescue species. (1), its nucleotide sequence information and/or single nucleotide polymorphisms is useful as a molecular genetic marker. (1) can be used for modifying lignin biosynthesis and/or cellulose degradation in a plant to manipulate cell walls. (1) or its fragments are useful for isolating cDNAs and genes
                                                                                           mechanical stress tolerance, disease resistance, insect pest resistance, plant stature, leaf and stem colour. The present sequence represents a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes a nucleic acid (1) or its fragment encoding caffeoyl-CoA 3-O-methyltransferase (CCOAMT), cinnamyl alcohol dehydrogenase (CAD), caffeic acid O-methyltransferase (OMT),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 11; Fig 62; 436pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel nucleic acid encoding lignification and cellulase enzymes or their related enzymes useful for modifying lignin biosynthesis and cellulose degradation in plants to manipulate plant cell wall
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F5H; CELL; phenylalanine ammonia lyase; PAL; 4-coumarate:CoA ligase; 4CL; ryegrass; fescue species; molecular genetic marker; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      caffeoyl-CoA 3-0-methyltransferase; cinnamyl alcohol dehydrogenase; CAD; caffeic acid 0-methyltransferase; OMT; cinnamate-4-hydroxylase; C4H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-JUL-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                  encoding homologous proteins from the same or other plant species,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200226994-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lolium perenne LpPALa nucleotide sequence SEQ ID NO:140.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ammonia lyase (PAL) or 4-coumarate:CoA ligase (4CL) from perennial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cinnamate-4-hydroxylase (C4H), cinnamoyl-CoA reductase (CCR), peroxidase
(PER), cellulase (CELL), ferulate-5-hydroxylase (F5H), phenylalanine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Spangenberg G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-SEP-2000; 2000AU-0000419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lolium perenne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cellulase; enzyme;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lolium perenne; perennial ryegrass; plant; cell wall; lignification
                                               invention.
                                                                     Colium perenne (perennial ryegrass) nucleotide sequence from the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (AGRE-) AGRESEARCH LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cinnamoyl-CoA reductase; CCR; peroxidase; PER; ferulate-5-hydroxylase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sawbridge TI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   lignin biosynthesis; cellulose degradation; CCOAMT,
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CCGCCGCGCACAAAAACCGCATCACCGAATGCCGGTCATACCCGCTGTATCGCTTCGTGC 1205
                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHAACTACCCACTGATGCAGAAGATGCGGGGGGGGTGGGAGAGGAGGGGTGGGAGAAGG 1025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTCAATTTTCTGAGCTGGTTAACGATTTCTACAACAATGGATTACCATCGAATCTCTCCCC 1436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOGGOGTGTCCATGACACACACACTIGCCATTGCTGCATCGGCAAGCTCATGTTG 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CATTGATCGACGITTCCAGAAACAAAGCITTIACACGGTGGTAACIICCAAGGAACCGCAA 1316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CACACAAGCTGAAGCATCATCCCGGGACAGATCGAGGCGCGCAGCCATCATGGAGCACATCC
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                                                                            CATTGTCGATTGCAAACAGGATTAAAGCTTGCAGATCGTACCCGTTGTATAGGTTTGTAA 2096
                                                                                                                                                                                                                                                                                                        GTGAGGCTCAGCGGCATGTGCAGACCTCAGTGTTCGGCGAAGCTCGGCGGCATTCGAGCAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCACATACCCATTAATGCAGAAGCTCCGACAGGTTCTGGTCGACCACGCTCTAAACAACG 1916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAAAGGTCCTCACCATGGGCGTCAACGGCGAGCTCCACCCGTCGAGATTCTTGCCAGAAAG 1796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCGACATCTTAAAACTCATGTCGTCGACATAGTTAGTCGACTCTATGCCAATCCATCGATTT 1676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTIGGGCGCAACCCGAGCTTTGGACTATIGGCTTTGAAGGGTTGCTTGAGATTTGCCATTGGCCTTCCTI 605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COCAGTIOTICCGAGOTAGIIGAACGACITICTACAACAATIGCTTTICCCTTTCCAATICTICTCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGTACGTAAGCGATTACGCCAAAGGCGCAAAAGGTCCACGAAATGGACCCGTTACAGA 1136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CACACAAATTGAAGCATCACCCTGGTCAAATCGAGGCGGCGGCGGCGATCATGGAGTATATTT 1076
                                                                                                                                                                                                                                                                                                                                                                                GCGAAACGGAGAAGAACACTAACACCTCCATCTTCCAAAAGATCGCTACCTTCGAAGAAG 1976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACCITGCITCCITGACGATICGACCGY RAGGCCGTGTTTCGCCTACGCAGAYGACCCTTGCAGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATCTCCTCCGTGTTGATCGTGAAATACGTCTTCGCTTACATCGACGACGACGTTTGCAGCG 1856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOTGCCATUTTGAGGAGAATGTTAGGGGTGCUTTGAAGAATTGTGTGAAGATGGTGGCAA 845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TACGCCATTTTGGAAGAGAACATGAAATCGACAGTGAAGAACACCGTAAGCCAAGTCGCGA 1736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOGACATTTTTGAAGCTCATGTCCTCGACATTCTTTGGTCGCCCTGTGCCCAGGCTATTCGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AACACAATICAAGACGITTAATTCTICTICGGATTIAATTTICAGCGAGGAAAACCGCAGAAGCAG 1616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACTGCTCC/AAGCTC/AATTCTTGGGCAACCCCGTGACTAACCATGTGCAGAGTGCGGAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOGGAGTIT FOR AT GGAC AAC ACCEGIT CITCGCC ATT TGCTGCAAT CGGAAAACT CATGTTCG 1376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CACTCATTGATGTCTCCCGAGGCAAGGCCATCCACGGTGGCAACTTCCAGGGCACTCCCCA 425
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                                                                                                                                                        AGCTCCC16C6CTGC1TCCAAGGGAGGTCGAGTCAGCCCGGTGYGCCGTGGAGAATGGCA ] 1145
                                                                                                                                                                                                                            AATTGAAAGTCCTGTTACCGAAAGAAGTTGAAGGTGTTAGAATCGCTTTATGAGAATGATA 2036
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biosynthetic pathway, and for producing a plant having altered lighin content, composition and structure. They can be used for designing probes and primers useful for detecting similar DNA and RNA sequences in any
                                                           polynumbed ides can be used for modulating lighth content, lighth composition and the structure of a plant, especially eucalyptus and pine species, and for modifying the activity of an enzyme involved in lighth
                                                                                                                       (CCP) phenylalanine ammonia-lyase (FAL), 4 coumarate:COA liquide (4CL), conferol qlucosyl transferase (CGP), conferon beta-qlucosidase (CBB), laccase, peroxidase, froulate-5-hydroxylase (FSH), alpha-anylase, caffere acid methyl transferase, caffeoyl FOA methyl transferase, coumerate COA liguides, cytochrome P450 lixiA, diphenol oxidase, flavanol glucosyl transferase, tlavenoid hydroxylase, and isoliavone reductase, which are involved in the liquid biosynthetic pathway. The
                                                                                                                                                                                                                                                                       encoding and representing the enzymes cinnamate 4-hydroxyiase (C4H), commarate 3-hydroxylase (C3H), phenolase (PNL), 0-methyl transferase (OMT), cinnamyl alcohol dehydrogenase (CAD), cinnamoyl-CoA reductase
                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 132-133; 213pp; English
                                                                                                                                                                                                                                                                                                                                     The present invention describes isolated polynucleotides and proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel polynucleotide encoding enzymes involved in lignin-biosynthetic pathway useful for producing transgenic plants especially cucalyptus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-317962/27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-UCT-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pinus radiata PAL nucleotide sequence SEQ ID NO:247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAA68154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAA68154 standard; DNA; 1520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1386 AAWAAAADACTTSAGARTYCAGAAGGYTYCACATGTGCTTAGTTAATWAGTAYAGT 1441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2097 - Gasalsia Grantasia Agamas IIIII isa masa Ga\Delta \Delta \Delta Gatasa Grantasia Grantasia 2156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (FLET-) FLETCHER CHALLENGE FORESTS LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GENE-) GENESIS RES & DEV CORP LID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               pine species having altered lignin content, composition and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IGGACANGSTGTTTGTGGGCATGAACAAGAGGGGAAACACATGAACGACGGCTGCTTGACTGCCTTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PTOGAGGGTGGAATGGGGAAGGTTTTTGGAATATGTTAGGAAAGTGAGTGTGAAAGCGTTT 2276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOJACAGGTGTTCACGGCGATGTGCAAAGGTCAAATIAIIGATCCGITGITGGAGTGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Havukkala IJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              lignin biosynthetic pathway, Bucalyptus grandis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99US-0143811
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organism and for PCR amplification. The lignin content can be efficiently modified using the polynucleotides. AAA67908 to AAA68201 and AAB16341 to AAB16449 represent polynucleotide and protein sequences used in the exemplification of the present invention.
1614 CAGTOGACATOTTAAAACTCATGTCGTCGACATACTTAGTCGCTCTATGCCAATCCATCG 1673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1554 AACAACACAATCAAGACGTTAATTCTCTCGGATTAATTTCAGCGAGGAAAAACCGCAGAAG 1613
                                                                                                                                                                                                                                                                                                                                                                 1434 CCGGTGGACGTAACCCTAGTTTGGACTACGGGTTCAAAGGTGGAGAAATCGCCATGGCTT 1493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1374 TCGCTCAATTTTCTGAGCTGGTTAACGATTTCTACAACAATGGATTACCATCGAATCTCT 1433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1134 AGAAACCAAAACAAGATCGTTATGCTCTCCGTACATCTCCCCAATGGCTCGGACCTCAAA 1193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1254 ACCCATTGATCGACGTTTCCAGAAACAAAGCTTTACACGGTGGTAACTTCCAAGGAACCC 1313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1194 TCGAAGTAATCCGATCATCAACCAAAATGATCGAGAGGGAAATCAATTCCGTCAACGACA 1253
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                                                                                                                                     837 AACAGCATAACCAGGATGTCAATTCTCTGGGTCTCGTTTCAGCTAGAAAATCTGCCGAGG 896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  717 GTGGTGGGCCTAATCCCAGCCTGGATTATGGACTGAAAGGGGCCGAGATCGCTATGGCTT 776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        657 TCGCTCAATTCTCAGAGCTTGTGAATGATTACTACAATGGAGGCTTGCCTTCGAATCTGA 716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    597 CTATTGGTGTTTCCATGGATAATCTTCGTCTGTCAATTTCAGCAATTGGGAAATTGATGT 656
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                                                                                                                                                                                                                                                                                                                 CTTACACTTCTGAGCTTCTTTACCTGGCAAATCCTGTCACCAGCCATGTACAGAGCGCCC 836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATCCAGTAATTGATGTTGCCAGAGACAAAGCTCTACATGGAGGGAATTTCCAGGGCACAC 596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGGAGATTATCAGATCTGCAACTCACATGATTGAGCGGGAAATCAATTCTGTGAATGACA 536
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TAACTCACAAGCTGAAGCACCATCCTGGCCAAATGGAAGCTGCAGCGATCATGGAGTATG 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAGTAATCTCTGCCATGTTCTGCGAGGTTATGAATGGGAAGCCTGAGTTTACAGATCCAT 297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 6.2e-106
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QY Вр QΥ B 29 Вþ QY ₽ 9 밁 δÃ Dβ 9 밁 Ş 8 1914 ACGGCGAAACGGAGAAGAACACTAACACCTCCATCTTCCAAAAGATCGCTACCTTCGAAG 1973 1377 TGAGAAACCAGCTCGGTA 1394 2094 TAAGGGAGGAGCTCGGCA 2111 1317 GGACCAGCCCTCTGCCCAACAGGATCCAGGAATGCAGGTCTTATCCTCTCTATGAATTTG 1376 2034 ATACATTGTCGATTCCAAACAGGATTAAAGCTTGCAGATCGTACCCCGTTGTATAGGTTTG 1257 CCGAGCTGAAGGCACAGCTTGAACCGCAAGTTAGTCTGGCCAGAGAAAGTTATGACAAAG 1316 1974 AAGAATTGAAAGTCCTGTTACCGAAAGAAGTTGAAGGTGTTAGAATCGCTTATGAGAATC 1137 ATGCCAGCTACCCATTGACTCAGAAACTGAGAAACATCCTGGTGGAACATGCCTTCAAGA 1196 1854 GCGGCACATACCCATTAATGCAGAAGCTCCGACAGGTTCTGGTCGACCACGCTCTAAACA 1913 1077 AGGATTTGCTCCAGGTAGTGGATAACGAACATGTTTTCTCTTACATTGACGATCCGTGCA 1136 1794 AAGATCTCCTCCGTGTTGTTGATCGTGAATACGTCTTCGCTTACATCGACGACGTTTGCA 1853 1017 CCAAGAAAACCCTGAGCACAGGGCTCAACGGGGAGCTTTTGCCAGGCCGTTTCTGCGAAA 1076 1734 ОБАЛАЛА БЕТОСТОЛО САТЕВЕСЕТОЛА ОБЕСЕЛЕНИЕ СЕТОВА СТОТОВ СТОТ 1674 ATTTACGCCATTTGGAAGAACATGAAATCGACAGTGAAGAACACCGTAAGCCAAGTCG 1733 957 ATTTAAGGCATCTGGAGGAAAACATGCTGGCCACTGTGAAGCAGATTGTTTCTCAGGTAG 897 CCATCGATATTCTGAAGCTGATGCTCTCCACATACCTGACAGCTCTGTGCCAGGCTGTGG ACGCAGAAGGTGAGAAGGATCCCAACACTTCCATTTTCAATAAGATTCCTGTGTTTGAAG 1016

Search completed: March 28, 2003, 21:56:09 Job time: 556 secs

GenCote version $5 \pm 4_{\rm LP} 5_{\rm L} 4578$ Copyright (c) 1993 ± 2003 Compugen Ltd

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Database
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Minimum DB seq length: 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Scoring table
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Perfect score.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
                                                                                                                                                                                                                                                                                                                                                                                                                                        A_Graceseq_101002.*

1. /SIDS2/rejidata/jerneseq/armeseqp-embl/AA1986 :A1.*

2. /SIDS2/gradata/gerneseq/armeseqp-embl/AA1981.LA1.*

3. /SIDS2/gradata/gerneseq/armeseqp-embl/AA1982.DAT.*

3. /SIDS2/gradata/gerneseq/armeseqp-embl/AA1984.EAT.*

5. /SIDS2/gradata/gerneseq/armeseqp-embl/AA1984.DAT.*

6. /SIDS2/gradata/gerneseqy-gerneseqp-embl/AA1985.DAT.*

6. /SIDS2/gradata/gerneseqy-gerneseqp-embl/AA1985.DAT.*

7. /SIDS2/gradata/gerneseqy-gerneseqp-embl/AA1987.DAT.*

8. /SIDS2/gradata/gerneseqy-gerneseqp-embl/AA1987.DAT.*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       March 28, 2003, 23.41.56 , Scarch time 67 Seconds (without alignments) 1414.048 Million cell updates/sec
908470 seqs, 133250620 residues
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Listing first 45 summaries
                                                                                                                                                                   /SIDS2/qcqdata/qeneseq/qeneseqp-emb1/AA1989.DAT:*
/SIDS2/qcqdata/qeneseqy-qeneseqp-emb1/AA1990.DAT:*
/SIDS2/qcqdata/qeneseqy-qeneseqp-emb1/AA1991.DAT:*
/SIDS2/qcqdata/qeneseqy-qeneseqp-emb1/AA1991.DAT:*
/SIDS2/qcqdata/qeneseqy-qeneseqp-emb1/AA1993.DAT:*
/SIDS2/qcqdata/qeneseqy-qeneseqp-emb1/AA1993.DAT:*
/SIDS2/qcqdata/qeneseqy-qeneseqp-emb1/AA1995.DAT:*
/SIDS2/qcqdata/qeneseqy-qeneseqp-emb1/AA1995.DAT:*
/SIDS2/qcqdata/qeneseqy-qeneseqp-emb1/AA1995.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                  /SIDS2/gcgdata/geneseg/genesegp-embl/AA1988.DAT:*
                                                                              /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1997.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1998.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1999.DAT:*
/SIDS2/qcqdata/qeneseq/geneseqp·embl/AA2002.DAT.*
                         /SIDS2/gcqdata/geneseq/geneseqp.embl/AA2000.DAT:*
/SIDS2/gcqdata/geneseq/geneseqp.embl/AA2001_DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution

Result	Score	Query Match	Length DB		ID	Description
1	3644	100.0		23	AAU97130	Lettuce LsPAL1
ŧJ	3294	90.4		ز ۱ ندا	MU97131	Lettuce LsFAL2
ىد	3059.5	84.0		14	AAR30077	Pisium sativum L P
4	3045.5	83.6		ڊ. د.	AAC36709	Ar
'n	3044.5	83.5		21	AAG36710	Arabidopsis
6	3041.5	83 5	698	21	VV38211	۸re
7	3004	82.4		21	AAG54103	Arabidopsis thalia
8	3004	82.4		12	AAG54102	۸ra
ç	2951	81.0		۲,	AAC54104	Ara
10	2907.5	79.8		2	AAC53399	Arabidopsis

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971.5	5.075	984.5	944.5	J. T.	987.5	987.5	988	990.5	990.5	991.5	991.5	991.5	991.5	991.5	992.5	992.5	994.5	994 5	994 5	994 5	994.5	994.5	3 366	1025	1337	1345	1475	1709	1752	1779	1799	1892	2548	2807
26.7		27.0	27.0		•			•				27.2						27 7	27.3	27 7	27.3	27.3	27.3	28.1	36.7		0	46.9	4 tb	48.8	49.4	51.9	72.7	77.0
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ABB07692	AAE2:0658	AAE20711	AAE29551	AAFLUEEE	AAEJU658	AAR70682	AAE20657	AAE20662	AAE20660	AAE16390	AAE20668	AAE20667	AAE20659	AAE20654	AAE20665	AA1:95783	AAF16389	ABP07693	AAE20653	AAP81099	AAP83141	AAP80513	AAE20664	ABB07690	AAU12066	AAB16404	ABB78983	AAG21949	AAC21948	ABB78982	AAB16402	AAG21947	AAC53401	AAG53400
					k. glutinis phenyl	Stabilised phenyla	Rhodotorula glutin	Rhodotorula glutin					Rhodotorula glutin		W. glutinis phenyl	L-phenylalanine am	Rhodotorula glutin	R. toruloides PAL	Rhodotorula glutin	Sequence of Rhodos	Sequence of L-phen	L-phonylalanine am	E. Glutinis phenyl	R. graminis PAL po	Protein encoded by	Pinus radiata PAL	Lolium perenne LpP	Arabidopsis thalia	Arabidopsis thalia	Lolium perenne LpP	ت			Arabidopsis thalia

ALIGNMENTS

RESULT 1 AAU97130

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Novel polynucleotide useful in preparing plant expression constructs to modify the response of a plant cell to wounding, damage or other injury	WFI: 2002-435152/46. N-PSDB: ABK50679.	Saltveit M, Campos R, Nonogaki H, Suslow T;	(REGC) UNIV CALIFORNIA.	26-SEP-2000; 2000US-235956P.	26-SEP-2901; 2001WO-US30192.	04-APR-2002.	W0200225028-A2	Lactuca sativa.	enzyme.	Lettude; phenylalanine ammonia-lyase; plant wounding; plant damage; plant disease; plant browning; vegetable crop; plant (LSPART)	Lettuce LsPAL1 enzyme.	13-AUG-2002 (first entry)	AAU97130;	AA097130 Standard; Protein; 711 AA.

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AAU97131 standard; Protein; 712 AA
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                                                                                                                                                  EELGRGFLTGEKVTSPGEEFDRVFTAMCKGQIIDPLLECLGGWNGEPLPIC 711
                                                                                                                                                                                                                                                                                                       KVLTMGVNGELHPSRFCEKDLLRVVDREYVFAYIDDVCSG1YPLMQK1.KQVLVUHALNNG
                                                                                                                                                                                                                                                                                                                                                                    HNQDVNSLGLISARKTAEAVDILKLMSSTYLVALCQSIDLRHLEENMKSTVKNTVSQVAK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QFSELVNDFYNNGLPSNLSGGRNPSLDYGFKGGEIAMASYCSELQFLANPVTNHVQSAEQ 480
                                                                                                         EELGRGFLTGEKVTSPGEEFDRVFTAMCKGQIIDPLLECLGGWNGEPLPIC 711
                                                                                                                                                                                             ETEKNTNTSIFQKIATFEEELKVLLPKEVEGVRIAYENDTLSIPNRIKACRSYPLYRFVR
                                                                                                                                                                                                                                        ETEKNTNTSIFQKIATFEEELKVLLPKEVEGVRIAYENDTLSIPNRIKACRSYPLYRFVR 660
                                                                                                                                                                                                                                                                                KVLTMGVNGELHPSRFCEKDLLRVVDREYVFAYIDDVCSGTYPLMQKLRQVLVDHALNNG
                                                                                                                                                                                                                                                                                                                                                                                                          HNQDVNSLGLISARKTAEAVDILKLMSSTYLVALCQSIDLRHLEENMKSTVKNTVSQVAK 540
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    \tt HKLKHHPGQIEAAAIMEYILDGSDYVKAAQKVHEMDPLQKPKQDRYALRTSPQWLGPQIE
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Pred. No. 2.3e-283;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Saltveit M,
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                                                                       The sequence is that of phenylalanine ammonia lyase (PAL) from Pisum sativum L. The gene encoding PAL may be used to produce PAL recombinantly. Plants contg. the PAL gene can
                                                                                                                                                                                    New phenylalanine ammonia lyase gene from Pisum sativum Laplasmid contg. gene, and E. coli transformed with plasmid,
                                                                                                                                                                                                                                        N-PSDB; AAQ31985
                                                                                                                                                                                                                                                                                                                                                                                                                                               Pisum sativum
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                               Sequence
                                                               contain a large amt
                                                                                                                                         Disclosure; Page 7; 9pp; Japanese.
                                                                                                                                                                          prepn. of lyase
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Query Match

DB 14;

Length 777;

25-FEB-2000; 2000EP-0301439

06-SEP-2000.

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Hest Local Similarity 83.8%; Pre
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                                                                                                                                                                                        hybridisation assay; genetic mapping; gene expression control; promoter;
                                                                                                                                                                                                                 Protein identification; signal transduction pathway; metabolic pathway;
                                                                                                                                                                                                                                                        Arabidopsis thaliana protein fragment Sky ID No: 45026
                                                                                                                                                                                                                                                                                                                                                                                         AAG36709 standard; Protein; 725
                                                                                       EP1033405-A2
                                                                                                                              Arabidopsis thaliana
                                                                                                                                                                       termination sequence.
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37: Mismatches 51,
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18 - OCT - 1999;

21 - OCT - 1999;
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                                                               RLATAATGKIMFAQFSELVNDFYNNGLPSNLSGGRNPSLDYGFKGGFTAMASYCSELQFL
                                                                                                                                               LRTSPOWLGPOLEVIRSSTKMIEREINSVNDNPLLDVSRNKALHGGNFOGTPIGVSMDNT
                                                                                                                                                                                                                              VMQGKPEFTDHLTHKLKHHPGQIEAAAIMEYILDGSDYVKAAQKVHEMDPLQKPKVDRYA
                                                                                                                                                                                                                                                                                        TAREAFKLAGISSCFFDLQPKEGLALVNGTAVGSGMASMVLFETNVLSVLAEILSAVFAE
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                                                                                                                                                                                                                                                                                                                                                                                                              GIRFEILEAITKFLNNNITPCLPLRGTTTASGDLVPLSYIAGLLTGRPNSKAVGPTGEVL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VVKLGGETLTVSÖVAGTAAANDSDTVKVELSEAAKAGVKASSDWVMESMNKGTDSYGVET 107
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                                                                                                                                                                                                        VMSGKPEFTDHL/THRLKHHPGQ1EAAA1MEH1LDGSSYMKLAQKLHEMDPLQKPKQDRYA
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                                                                                                                         LRTSPQWLGPQIEVIRYATKSIEREINSVNUNPLILVSFNKAIHGGNEGGIFIGVSMUNT
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81.4%; Fred. No. 2.5e-235;
Live 52, Mismatches 66;
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14 - MAY - 1999
18 - MAY - 1999
19 - MAY - 1999
20 - MAY - 1999
21 - MAY - 1999
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04-MAY-1
05-MAY-1
06-MAY-1
06-MAY-1
11-MAY-1
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09-MAR 1999
23-MAR 1999
25-MAR 1999
26-MAR 1999
01-AFR 1999
01-AFR 1999
01-APR 1999
16-APR 1999
16-APR 1999
21-APP 1999
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RESULT 6
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                                                                                                 termination sequence.
                                                                                                                         hybridisation assay; genetic mapping; gene expression control; promoter;
                                                                                                                                                        Protein identification; signal transduction pathway, metabolic pathway;
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Similarity 83.1%; Pred. No. 2.9e-235;
85, Conservative 52, Mismatches 62, Indels 5,
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                                PLRGTITASGDLVPLSYTAGLLTGRPNSKAVGPTGEVLNAEKAFAAAAGVEGGFFELQPKE
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28-00T-1999;
28-00T-1999;
29-00T-1999;
Arabidopsis thaliana
                                                                                                                                                                           AAG54102
                          termination sequence
                                                                                   Arabidopsis thaliana protein fragment SEQ ID NO: 68948.
                                                                                                                  18-OCT-2000
                                         hybridisation assay; genetic mapping; gene expression control; promoter;
                                                       Protein identification; signal transduction pathway; metabolic pathway;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QTELIRFLNAGIFGNTKETCHTLPQSATRAAMLVRVNTLLQGYSGIRFEILEAITSLLNH
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DVNSLGLISSRKTSEAVDIIKLMSTTFLVGICQAVDLRHLEENLRQTVKNTVSQVAKKVL
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                                                                                                                                                                                                                                                   GTKLLTGEKVVSPGEEFDKVFTAMCEGKLIDPLMDCLKEWNGAPIPIC
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                                                                                                                                                                                                                                                                                                                                      KNTNTSIFQKIATFEEELKVLLPKEVEGVRIAYENDTLSIPNRIKACRSYPLYRFVREEL
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                                                                                                                (first entry)
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99US-0161993.
99US-0162142.
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81.5%;
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18-AUG 1999 20-AUG 1999 20-AUG 1999 20-AUG 1999 20-AUG 1999 23-AUG 1999 23-AUG 1999 25-AUG 1999 26-AUG 1999 27-AUG 1999 27-AUG 1999 30-AUG 1999 31-AUG 1999

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28-SEP-1999
04-OCT-1999
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14-OCT-1999
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370 QATKSIEREINSVNDNPLIDVSRNKAIHGGNFQGTPIGVSMDNTRLAIAAIGKLMFAQFS
       364 SSTKMIEREINSVNDNPLIDVSRNKALHGGNFQGTPIGVSMDNTRLAIAAIGKLMFAQES 423
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                                       KHHPGQIEAAAIMEYILDGSDYVKAAQKVHEMDPLQKPKQURYALKISPQWLGPQIEVIK
                                                                                                              NITPCLPLRGTITASGDLVPLSYIAGLLTGPPNSKAVGPTGEVLNAEKAFAAAGVEGGFF
                                                                                                                              QTELIRFLNAGIFGNTKETCHTLPQSATRAAMLVFVNTLLQGYSGIRFEILEAITSLLNH
                                                                                                                                      QKELLIRELNAGIEGNGIEISHILPHSATKAAMIVKINILLQGYSGIKFEILEAITKFLNN
                                                                                              KHHPGQIEAAAIMEHILDGSSYMKLAQKVHEMDPLQKPKQDRYALRTSPQWLGPQIEVIR
                                                               DLQPKEGLALVNGTAVGSGMASMYLFEANVQAVLAEVLSAIFAEVMSGKPEFTDHLTHKL
                                                                               ELQPKEGLALVNGTAVGSGMASMVLFDANVLALLSEVLSAIFAEVMQGKPEFTDHLTHKL
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577; Conserva
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990S-0161405
990S-0161406
990S-0161356
990S-0161356
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99US-0154779.
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81.5%; Pred. No. 5.2e-232;
Mismatches 77;
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                                                                                Arabidopsis thaliana protein fragment SEQ ID No: 67982
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay, genetic mapping, gene expression control; promoter; termination sequence.
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Novel polynucleotide encoding enzymes involved in lignin-biosynthetic
                                WP1; 2000-317962/27.
                                                            Bloksberg I.N. Havukkala IJ
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transferase (OMT), cinnamyl alcohol dehydrogenase (CAD), cinnamy
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                                                                                                                                                                                                                                                                         Claim 18; Fage 170:171, 213pp, English.
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420 KI.MFA 424
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                                                                                                                                                                           416 KIMFA 420
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                                                                                                                                                                                                                                                                                                                                              360 GPQIEVIRAATKMIEREINSVNDNPLIDVARNKALHGGNFQGTP1GVSMDNTRLAVASIG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TDHLTHKLKHHPGQIEAAAIMEYILDGSDYVKAAQKVHEMDPLQKPKQDRYALRTSPQWL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cinnamoyl-CoA reductase; CCR, peroxidase, PER, ferulate:5 hydroxylase; F5H; CELL; phenylalanine ammonia lyase; PAL; 4-coumarate:CoA ligase; 4CL; ryegrass, fescue species; molecular genetic marker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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their related enzymes useful for modifying lignin biosynthesis and
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cinnamate-4-hydrogenase; CAL; caffeic acid O-methyltransferase; OMT; cinnamate-4-hydrogenase; CAL; caffeic acid O-methyltransferase; OMT; cinnamate-4-hydrogenase; CAL; caffeic acid O-methyltransferase; caffeic acid O-methyltransfer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lolium perenne; perennial ryegrass; plant; cell wall; lignification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lolium perenne LpPALa amino acid sequence SEQ ID No:141.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 biosynthesis and/or cellulose degradation in a plant to manipulate cell walls. (I) or its fragments are useful for isolating cDNAs and genes
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                                                                                                                                                                                                                                                                                                                                                                                                               Lolium perenne.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       invention
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                                                                                       323 SDYVKAAQKVHEMDELQKEKQDRYALKTSEQWLGEQIEVIRSSTKMIEREINSVNDNELI 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         263 MASMVIFDANVLALLSEVI.SAIFAEVMQGKPEFTDHLTHKIKHHPGQIEAAAIMEYILDG 322
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Search completed. March 29, 2003, 02:10:05
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Result
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Sequence 327, App
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PRIOR FILING DATE: 1997 11·21
PRIOR APPLICATION NUMBER: US 08
PRIOR APPLICATION NUMBER: US 09
PRIOR FILING DATE: 1996-09-11
PRIOR APPLICATION NUMBER: US 09
PRIOR FILING DATE: 1998-10·09
Sequence 13, Application US/09624693A Patent No. 6355468 GENERAL INFORMATION:
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Best Local
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APPLICANT: Havukkala, Ilkka
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ORGANISM: Pinus radiata
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UMBER: US 09/169,789
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Yoshida, Roberta
APPLICANT: Kootstra, Anna
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675 EELGVQARRGDVFVGVQQETIGSNVSRIYEAIKDGRINHVLVKML 719
                                                                                                                             618 SANVTLTAVNAWKVASAEKAIS--LTREVRN-RFWQTPSSQAPAHAYLSPRTRVLYSFVR 674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            312 AAAIMEYILDGSDY-VKAAQKVHEMDPLQKPKQDKYALKTSPQWLGPQIEVIKSSIKMIE 370
                                                           661 EELG----RG-FLTGEKVTSPGEEFDRVFTAMCKGQIIDPLLECL 700
                                                                                                                                                                                            602 TEKNTNTSI-FQKIATFEEELKVLLPKEVEGVRIAYENDTLSIPNRIKACRSYPLYRFVR 660
                                                                                                                                                                                                                                                           573 ALALEVKKALNKRLEQTTTYDLEPRWHDAFSY----ATGT------VVELLSSSP 617
                                                                                                                                                                                                                                                                                                                      549 G-ELHPSKECEKULLKVVUKEY-----VEAYIUUVCSGTYPLMQKLKQVLVUHALNNGE 601
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          394 LENNTTTUNPLLDVENKQTAHGGNFQASAVSISMEKTRLALALIGKLNFTQCTELLNAAM 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         371 REINSVNDNPLIDVSRNKALHGGNFOGTPIGVSMDNTRLAIAAIGKLMFAQFSELVNDFY 430
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      216 SASGDLSPLSYIAGAITGHPDVKVHVLHEGTEKIMFAREAISLFGLEA--VVI.GPKEGLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              196 TASGDLVPLSYTAGLLTGRPNSKA---VGPTGEVLNAEKAFAAAGVEGGFFELQPKEGIA 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                156 FSVGRGLENTLPLEVVPGAMVIPVNSLTRGHSAVRLVVLEALTNFLNHPITPIVPLRGSI 215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                83 AGYKASSDWYMESMNKGTDSYGYTTGFGATSHRRTKQGGALQKELIRFLNAGI-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NNGLPSNLSGGRNPSLDYGFKGGEIAMASYCSELQFLANPVINHVQSAEQHNQDVNSLGL 490
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US-09-624-693A-19; Sequence 19, Appli; Patent No. 6355468

Sequence 19, Application US/09624693A

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oucry Match 27.3%, Score 994.5, DB 4, Length 716;
Hest Local Similarity 35.9%; Pred. No. 4.9e-81;
Matches 270; Conservative 12%, Mismatches 250; Hidels 109; Gaps
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APPLICANT: Koolstra, Anna
TITLE OF INVENTION: Phenylalanine Ammonia tyase Polypeptide and
TITLE OF INVENTION: Polypucleotide Sequences and Methods of Obtaining and
TITLE OF INVENTION: Using Same
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TYPE: PRT
ORGANISM: Rhodotorula toruloides
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                                                                                                                                                                                                                                                                                                                                                                                                                                               482 GHLANPYTTHYQPAEMANQAVNSLALISARRTTESNDYLSLLLATHLYCVLQAIDLRAIE 541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            465 QFIANPYTNHVQSARQHNQDVNSLGLISARKTARAVDILKLMSSTYLVALCQSIDLRHLE 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           423 EKTRLGLAQIGKLNFTQLTEMLNAGMNRGLPSCLA-AEDPSLSYHCKGLDIAAAAYTSEL 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           405 DNTRLATAATGKLMFAQFSELVNDFYNNGLPSNLSGGRNPSLDYGFKGGETAMASYCSEL 464
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685 GKQEVTI-GSNVSKIYEAIKSGRINNVILKMI, 715
                                                 669 TGEKVTSPGEEFDRVFTAMCKGQIIDPLLECL 700
                                                                                                                                                           633 -RIAYENDTLSIPNRIK-----ACRSYP------LYRFVREELG----RG--FI, 668
                                                                                                                                                                                                                   566 GSNLRDELVE-KVNKTLAKRLEQTNSYDLVPRWHDAFSFAAGTVVEVLSSTSLSLAAVNA 624
                                                                                                                                                                                                                                                                       585 MQKLRQVLVDHALMNGETEKNTNTSTFQKTATFEEELKVLLPKEVEGV------ 632
                                                                                                                                                                                                                                                                                                                                                                                       525 ENMKSTVKNTVSQVAKKVLTMGVNGELHPSRFCEKDLLRVVDREYVFAYIDDVCSGTYPL 584
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                                                                                                         625 WKVAAAESATSLTROVRETEWSAASTSSPALSYLSPRTQILYAFVREELGVKARRGDVFL 684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        363 YPLRTSPOWLGPLYSDLIHAHAVLTLEAGOSTTONPLLDVENKTSHHGGNEQAAAVANTM 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   288 VMQGKP-EFTDHLTHKLKHHPGQIEAAAIMEYILDGSDY-VKAAQKVHEMDPLQKPKQDR 345
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	NA 624	MVLKVVLVADRALNNASLENNINIS JEQALATEREELA VELVEKVEGAV GSNLKDELVE: KVNKTLAKKUEÖJNSYDLVFKWHDAFSFAAGI VVEVLSSISISIAAVNA	566	D 4	
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		ENMKSTYKNTYSQVAKKVLIMGVNGELHESREGEKDLLRVVDREYVFAYIDDVCSGTYPL FEEKK	5 2 5 4 2 5	nh Qy	
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	SM 404 :- IIM 422	THE CONTROL OF THE PROPERTY	363 405	c B 2	
		VMOGKP-EFTDHLTHKLKHHPGOLEAAAIMEYILDGSDY-VKAAOKHEMDPLOKPKODK THE CONTROL OF THE	288 303	P P P	
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	VI. 227 :	FEILEAITKFLNNNJTPCLPLRGTITASGDLVPLSYIAGIL/TGKPNSKA-VGPTGEVL 	171 185	Ωу	
	IK 170 :- VR 184	GGALQKELIRFLNAGIFGNGTETSHTLPHSATRAAMIVKINTILQGYSGIK	120 127	qq VQ	
	KQ 119 : ED 126	QVAGIAAANDSDTVKVELSEAARAGVKASSDWVMESMNKGTDSYGVTTGFGATSHRRTKQ 	60 71	Qу	
	VS 59 : 1.G 70	NGVVNELCIKDPLNMGVAAEALTGSHLDEVKKMVAEERKPVVKLGGELLTVS 	8 1 4	Qy Db	
hai wai	Gapa	Query Match 27.3%; Score 994.5; DB 4; Length 716; Best Local Similarity 35.9%; Pred. No. 4.9e-81; Matches 270; Conservative 123; Mismatches 250, Indels 169,	ery M est Lo atches	Ma Ma	
		US-09-627-216A-8 Sequence 8, Application US/09527216A PALENT NO. 6368837 GENERAL INFORMATION: APPLICANT: Sariasiani, Sima F APPLICANT: Sariasiani, Sima F APPLICANT: Tang, Xiao-Song AFFLICANT: Vannelli, Todd APPLICANT: Vannelli, Todd APPLICANT: Gatenby, Anthony TITLE OF INVENTION: Bioproduction of para-Hydroxycinnamic Acid FILE REFERENCE: HC1009 US NU FILE REFERE	99-627 equent NERAL APPLICO,	C	
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 27.2%; Score 991.5; DB 4; Length 716; Best Local Similarity 35.9%; Pred. No. 9.2e-81; Matches 270; Conservative 122; Mismatches 251; Indels 109; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Microsoft Office 97
SEQ ID NO 10
LENGTH: 716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Gatenby, Anthony
TITLE OF INVENTION: Bioproduction of para-Hydroxycinnamic Acid
FILE REFERENCE: BC1009 US NA
CURRENT APPLICATION NUMBER: US/09/627,216A
CURRENT FILING DATE: 2000-07-27
PRIOR APPLICATION NUMBER: 60/147,719
PRIOR FILING DATE: 199-08-06
NUMBER OF SEQ ID NOS: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 10, Application US/09627216A Patent No. 6368837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Sariaslani, Sima F
APPLICANT: Tang, Xiao-Song
APPLICANT: Qi, Wei Wei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Description of Artificial Sequence: mutant from OTHER INFORMATION: Rhodtorula glutinis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
465 QFLANPVTNHVQSAEQHNQDVNSLGLISARKTAEAVDILKLMSSTYLVALCQSIDLRHLE 524
                                                        423 EKTRLGLAQIGKLNFTQLTEMLNAGMNRGLPSCLA-AEDPSLSYHCKGLDIAAAAYTSEL 481
                                                                                                                                                                  363 YPLRTSPQWLGPLYSDLIHAHAVLTIEAGQSTTDNPLIDVENKTSHHGGNFQAAAAVANTM 422
                                                                                                                                                                                                                                                                                                                   288 VMQGKP-EFTDHLTHKLKHHPGQIEAAAIMEYILDGSDY-VKAAQKVHEMDPLQKPKQDR 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                171 FEILEAITKFLNNNITPCLPLRGTITASGDLVPLSYIAGLLTGRPNSKA-VGPTG--EVL 227
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                                                                                                             405 DNTRLAIAAIGKLMFAQFSELVNDFYNNGLPSNLSGGRNPSLDYGFKGGEIAMASYCSEL 464
                                                                                                                                                                                                                             346 YALRTSPQWLGPQI-EVIRSSTKMIEREINSVNDNPLIDVSRNKALHGGNFQGTPIGVSM 404
                                                                                                                                                                                                                                                                                  303 AMVGHAGSFHPFLHDVTRPHPTQIEVAGNIRKLLEGSRFAVHHEEEVKVKDDEGILRQDR 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                        228 NAEKAFAAAGVEGGFFELQPKEGLALVNGTAVGSGMASMVLFDANVLALLSEVLSAIFAE 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                185 LVVLEALTNFLNHGITPIVPLRGTISASGDLSPLSYIAAAISGHPDSKVHVVHEGKEKIL 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             127 AISLQKALLEHQLCGVLPSSFDSFRLGRGLENS--LPLEVVRGAMTIRVNSLTRGHSAVR 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               685 GKQEVTI-GSNVSKIYEAIKSGRINNVLLKML 715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 669 TGEKVTSPGEEFDRVFTAMCKGQIIDPLLECL 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      625 WKVAAAESAISLTRQVRETFWSAASTSSPALSYLSPRTQILYAFVREELGVKARRGDVFL 684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14 NGVAS---AKQAVNGASTNLAVAGSHLPTTQVTQVDIVEKMLAAPTDSTLELDGYSLNLG 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          71 DV--VSAARKGRPVRVKDSDEIRSKIDKSVEFLRSQLSMSV--YGVTTGFGGSADTRTED 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60 QVAGIAAANDSDTVKVELSEAARAGVKASSDWVMESMNKGTDSYGVTTGFGATSHRRTKQ 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8 NGVVNELCIKDPLNWGVAAEALTGSHL------DEVKKMVAEFRKPVVKLGGETLTVS 59
                                                                                                                                                                                                                                                                                                                                                                                                  YAREAMALFNLEP--VVLGPKEGLGLVNGTAVSASMATLALHDAHMLSLLSQSLTAMTVE 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGALQKELIRFLNAGI-----FGNGTETSHTLPHSATRAAMIVRINTLLQGYSGIR 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vannelli, Todd
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	Db	482 GHLANPVTTHVQPAEMANQAVNSLALISARRTTESNDVLSLLLATHLYCVLQAIDLRATE 541
	Оу	RFCEKDLLRVVDREYVFAYIDDVCSG
	DЬ	542 FEFKK
	Qy	585 MQKLRQVLVDHALNNGETEKNTNTSIFQKIATFEEELKVLLPKEVEGV 632
	Db	DELVE-KVNKTLAKRLEQ
	ру	633 -RIAYENDTLSIPNRIKACRSYPLYRFVREELGRGFL 668
	0	69 TGEKVTSDGEEFDRVFTAMCKGOIIDDLLECL 700
	B 2	85 GKQEVTI-GSNVSKIYEAIKSGRINNVLLKML
	では	SULT 7 -09-624-693A-17 Sequence 17, Application US/09624693A
	 GP A H G	PARENT NO. 6359468 GENERAL INFORMATION: APPLICANT: Yoshida, Roberta APPLICANT: Kootstra, Anna
	 	TITLE OF INVENTION: Phenylalanine Ammonia Lyase Polypeptide and IITLE OF INVENTION: Polypucleotide Sequences and Methods of Obtaining and IITLE OF INVENTION: IIsing Same
÷	 z o o ¤	FILE REFERENCE: 29479/500NSC CURRENT APPLICATION NUMBER: US/09/624,693A CURRENT FILING DATE: 2000-07-24 NUMBER OF SEO ID NOS: 25
	; SE	EO ID NO 17 LENGTH: 713 TYPE: PRT ORGANISM: Rhodotorula mucilaginosa 09-624-93A-17
	м а	Query Match 26.7%; Score 971.5; DB 4; Length 713; Best Local Similarity 36.7%; Pred. No. 5.9e-79; Matches 267; Conservative 125; Mismatches 277; Indels 59; Gaps 22;
	Oy	MENGNHANGVVNELCI-KDPLNWGVAAEALTGSHLDEVKKMVAEF-RKPVVKLGGETLTV 5: :::: : :
	2 5	LONG THE TOWN THE TRANSPORT OF THE TRANS
	Дy	59 SQVAGIAAANDSDTVKVELSEAARAGVKASSDAVMESHKRGTDSYGVTTGFGATSHRRTK 118
	Qy	119 QGGALQKELIRFLNAGIFGNGTETSHTLPHSATRAAMIVRINTLLQGYSGI 169
	Db	132 DAISLQKALLEHQLCGVLPTSMDGFALGRGLENSLPLEVVRGAMTIRVNSLTRGHSAV 189
	Оy	170 RFEILEAITKELNNNITPCLPLRGTITASGDLVPLSYIAGLLTGRPNSKAVGPTGEVINA 229
	Db	190 RIVVLEALTNFLNHGITPIVPLRGTISASGDLSPLSYIAASITGHPDSK-VHVDGKIMSA 248
	Qy	230 EKAFAAAGVEGGFFELQPKEGLALVNGTAVGSGMASMVLFDANVLALLSEVLSAIFAEVM 289
	Db	249 QEATALKGLQPVVLGPKEGLGLVNGTAVSASMATLALTDAHVLSLLAQALTALTVEAM 306
	Qy	290 QGKP-EFTDHLTHKLKHHPGQIEAAAIMEYILDGSDY-VKAAQKVHEMDPLQKPKQDRYA 347
	Db	307 VGHAGSEHPFLHDVTRPHPTQIEVARNIRTLLEGSKYAVHHETEVKVKDDEGILRQDRYP 366
	Qy	348 LRTSPQWLGPQI-EVIRSSTKMIEREINSVNDNPLIDVSKNKALHGGNFQGTPIGVSMDN 406
	DЬ	367 LRCSPOWLGPLVSDMIHAHAVLSLEAGOSTTDNPLIDLENKMTHHGGAFMASSVGNTMEK 426

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 21, Application US/09624693A Patent No. 6355468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ 1D NO 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Yoshida, Roberta
APPLICANT: Koolistra, Anna
TITLE OF INVENTION: Phenylalanine Ammonia Lyase Polypeptide and
TITLE OF INVENTION: Polypucleotide Sequences and Methods of Obtaining and
TITLE OF INVENTION: Using Same
FILE REFERENCE: 29479/500NsC
CURRENT APPLICATION NUMBER: US/09/624,693A
CURRENT FILING DATE: 2000-07-24
NUMBER OF SPO ID NOS: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: SITE ICCATION: (12, 16, 17, 20, 24, 25, 28 + 30, 38, 42, 47, 48, 56, 57, 52, 66, OTHER INFORMATION: "Xaa" means any amino acid: "Xaa" means no consensus at that OTHER INFORMATION, position OTHER INFORMATION. Description of Artificial Sequence: Consensus of OTHER INFORMATION. SEQ ID NOS. 13, 17, and 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ENGTH: 726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         705 APVI.VKMM 712
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                646 SSSSPALKYLSPRTRVLYSFVREEVGVKARPGCVYLGKÇEVTI GINVSFIYEAIKSGCI 704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     641 LSIPHRIK--ACRSYPLYRFYREELG----RG--FUTGEKVTSPGEEFDRVFTAMCKGQ1 692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             486
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 427 TRLAVALMCKVSFTQLTEMI.NAGMNRALPSCLA-AEDPSLSYHCKGLD1AAAAYTSELGH 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              407 TRLAIAAIGKLMFAQESELVNUFYNNGLPSNLSGGRNPSLDYGFKGGELAMASYCSELQF 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  587 KLRQVL-----VDHALNNGETEKNTNTSIFQKIATFEEELKVLLPKEVEGVRIAYENDT 640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  527
223 SPLSYIAAAITHIFFISKUHVXHEHXEKIMXAFEAIALFHLEF VVLHPKEHIHLVNGTA 280
                                                                                                          165 NS--LPLEVVRGAMTIRVNSLTRGHSAVRLVVLEALTNFLNHGITPIVPLRGTISASGDL 222
                                                                                                                                                            142 TSHTLPHSATRAAMIVRINTLLQGYSGIRFEILEAHTKELNNNITPCLPLRGTITASGDL 201
                                                                                                                                                                                                                       107 FLRXQLXNSV--YGYTTGFGGSADTRTEDAISLQKALLEHQLCGVLPTSXDSFXLGRGLE 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          593 RWHDTESVATGAVVEALAGQEVSLASLNA--WKVACAEKAIAL-----TRSVRDSEWAAP 645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       546 HTKAFEPMVTELLKQHF-----GALATAEVEDK-----VRKSIYKRLQQ--NNSYDLEQ 592
                                                       202 VPLSYTAGLL/IGRPNSKA-VGPTG--EVLNAEKAFAAAGVEGGFFELQPKEGLALVNGTA 258
                                                                                                                                                                                                                                                                         91 WYMESMNKGTDSYGYTTGFGATSHRETKUGGALQKELIRFLNAGI-----FGNGTE 141
                                                                                                                                                                                                                                                                                                                                    49 TQLDIVEXXLADPXTDDXXELDGYSLTLGDVVG--AAPKGRXVRVXDSDEIRXKIDKSVE 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                         32 SHIDEVKKMVAE-FRKPVVKLGGETLTVSQVAGTAAANDSDTVKVELSEAARAGVKASSD 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MKSTVKNTVSQVAKKVLITMGVNGHLHPSKHCEKULLKVVUKBYVHAYIDDVCSGTYPLMQ 586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LANPVSTHVQPAEMGNQAINSLALISARRTAEANDVLSLLLATHLYCVLQAVDLRAMEFE 545
                                                                                                                                                                                                                                                                                                                                                                                                                                                 263; Conservative 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26.5%; Score 967; DP 4; Length 726; 36.9%; Pred No. 1 5e-78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches 262;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 indels 80;
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,F 13 14 14	VVDREYVFAYIDDVOSGIYPLMQKLROVLVDHALNNGETEKNTNTSIFOKIATFEEELKV	554	ić.
120		61	da
563	KLMSSTYLVALCQSIDLRIHLEBNMKSTVKNTVSQVAKKVLTMGVNGELIFPSRFCEKDLLR	504	27
503 60	PSLDYGFKGGELAMASYCSELOFLANPYTNHVOSAEOHNODVNSLGLLSAKKTAFAVDTI. 	444 ±	44
ps	y Maich 25 8%; Score 939, DR 4, Longth 226; Local Similarity 80 5%; Pred. No. 6.9e-77; hes 182; Conservative 19; Mismatches 25; Indels 0; Gaps	Query Ma Best Loc Matches	De:
	TYPE: PRT ORGANISM: Eucalyptus grandis 09-615-192A-327	TYPE: ORGANI 9-615-	; ; ;
	THE RESIDENCE ACTION OF THE PERSON OF THE PE	ENGT	SEG
	PRIOR FILING DATE: 1998-10-09 NUMBER OF SEQ ID NOS: 405 SOPTMARE: 1998-10-09	MHER MHER MHER MHER	 2 Z T
	PRIOM APPLICATION NUMBER - 03 08/714,000 PRIOM FILING DATE: 1496-09-11 PRIOM APPLICATION NUMBER - 03 04/169,789	4 4018 4 4018 4 4018	 <u></u>
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	T APPLICATION NUMBER: US/09/615,192A	JRRENI	 2 <u>0</u> t
	PF INVENTION: Materials and Methods for the PRESENCE: 11000 1003-40		 च⊢⊟
	sberg, Leonard N. kkala, likka	701'1de 701'1de	 } <u>~ ~ :</u>
	RESULT 9 US-09-615-192A-327 ; Sequence 327, Application US/09615192A ; Patent No 6410718 ; Patent Autopartion	Juence	RESULUS - 01
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673	(XXXXVSLAAVNAWKVAXAEKAISLTRXVRXXFWXAPSSSSPALXYLSPRTK	614	Db
653		616	γy
613	XXXXELXXKVXKXLXKRLEQTNSYDLEPRWHDAFSXATG	575	Dβ
615	VEAYIDDVCSGTYPLMOKLROVLVDHALANGETEKNTNTSIFOKIA	556	Qy
574		520	G.
555	MGVNGELHPSR	496	Оу
519	SCLA-AEDPSLSYHCKGLDIAAAAYTSELGHLANPVITHVQPAFMGNQAVNSLALISARR	461	Db
495		436	Qy
460	TIDNPLIDVENKXTHHGGNPQASAVXNTMEKTRIALALIGKLNFTQLIEMLNAGMNRGIP	401	Db
435		376	Ϋ́
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375	Y LLDGSUY - VKAAQKVHEMDELQKEKQDRYALETSPOWLGPOT - EVTRSSTKMTERETINS	318	ÓΛ
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APPLICANT: Kootstra, Anna
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                                                                                                               ENMKSTVKNTVSQVAKKVLTMGVNGELHPS--RFCEKDLLRVVDREYVFAYIDDVCSGT- 581
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; Patent No. 6410718
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LENGTH: 164
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                                                                                                                                                                                                   APPLICANT: Bloksberg, Leonard N.
APPLICANT: Havukkala, Ilkka
TITLE OF INVENTION: Materials and Methods for the
TITLE OF INVENTION: Modification of Plant Lignin Content
FILE REFERENCE: 11000.1003c4U
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                                            PRIOR APPLICATION NUMBER: US
PRIOR ETLING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: US
PRIOR FILLING DATE: 1996-09-11
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APPLICANT:
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NUMBER OF SEQ ID NOS.
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Havukkala, Ilkka
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1998-10-09
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                                                                                                                                                                                              Sequence 331. Application MS/09615192A Patent No. 6410718
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SOFTWARE: FastSEQ for Wind
SEQ ID NO 329
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APPLICANT: Havukkala, Ilka
TITLE OF INVENTION: Materials and Methods for the
TITLE OF INVENTION: Modification of Plant Lignin Content
FILE REFERENCE: 11000.1003c4U
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                                                                                                                            APPLICANT: Bloksberg, Leonard N. APPLICANT: Havukkala, likka
                  CURRENT APPLICATION NUMBER: US/09/615,192A CURRENT FILING DATE: 2000-07-12
                                                             TITLE OF INVENTION: Materials and Methods for the TITLE OF INVENTION: Modification of Plant Liquin Content FILE REFERENCE: 11000 1003c4U
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SOFTWARE. FastSEC for Windows Version 3.0
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PRIOR APPLICATION NUMBER:
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TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                            242 FEELÖPKECLALVNGTAVGSGMASMVLFDANVLALLS 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 182 NNNITPCLPLRGTITASGDLVPLSYIAGLLTGRPNSKAVGPTGEVLNAEKAFAAAGVEGG 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         652 SYPLYREVREEL/PROFITGEKVTSPOREFORVETAMORGQIIOPLLECLOGMIG /05
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
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US 08/975,316
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US-09-268-347-36
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SEQ ID_NO 36
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LENGTH: 132
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Patent No. 6335182
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CURRENT APPLICATION NUMBER, US/09/258,347
CURRENT FILING DATE: 1999-03-16
NUMBER OF SEQ ID NOS: 54
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TITLE OF INVENTION RECOMBINANT HAEMOPHILUS INFLUENZAE ADHESIN PROJEINS
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PRIOR FILING DATE: 1996-09-11
PRIOR APPLICATION NUMBER: US 99/169,789
PRIOR FILING DATE: 1998-10-09
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                                                                                                                                                                                                                                                                                                                                                                                                                                  259 VGSGMASMVLFDANVLALLSEVLSATFAEVMQGKPEFTDHLTHKLKHHPGQTEAAATMEY 318
                                                                                                         572 GLLNLNEKNANKQPLVTDSTAATVGDLRKLGWVVSTKNGTKEESNQVKQADEVL-----F 626
                                                                                                                                                                                                                                                                      514 NGGTTGTNT1--SVTKDGIKAGNKAITNVASGLRAYDDANFDVLNNSATDLNRHVEDAYK 571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   396 GGKVAETAKEDDKKKLVNAGDLVTALGNLSWKAKAEADTDTDGALEGISKDQEVKAGETV 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               347 ESGDGTTASVT----KDTNGNGITVKYDAKVGDGLKFDSDKKIVAD-----TTALTVT 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58 VSQVAGIAA-----ANDSDTVKVELSEAARAGVKASSDWVMESMNKGTD-SYGVTT 107
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Local Similarity 20.7%; Pred. No. 0.34;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16 IKDPLNWGVAAEALTGSHLDEVKKMVAEFEKPVVKLGGETLTVSQVAGIAAANDSDTVKV 75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 ENGNHVNGVVNELCIKDPLNWGVA----AEALIGSHLDEVKKMVAEFRKPVVKLGGETLI 57
                                                   TGAGAATVISKSENGKHITITVSVAETKALSGLEKLGDTIKLKVDNQNTDNVLTVGNNGTA 686
                                                                                                                                                                                                                                                                                                                      GNGTETSHTLPHSATRAAM-----IVRINTLLQGYSGIRFEILEAITKFLNNNITPCL- 189
                                                                                                                                                                                                                ------PLRGTITAS--GDLVPLSYIAGLLTG-RPNSKAVGPTGEVLNAEKAF 233
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ch com	923	538	867	485	836	425	789	366	731	319	687
Search completed: March 29, 2003, 02:14:08 Job time : 43 secs	923 KADGKGADVKIGAKTSVIKDHNGKLFTGKDL 953	538 VAKKVLTMGVNGELHPSRFCEKDL 561	867 LNVDATKKSNAASIEDVLRAGWNIQGNGNNVDYVATYDTVNFTDDSTGTTTVTVTQ 922	485 VNSLGLISARKTAEAVDILKLMSSTYLVALCQSIDLRHLEENMKSTVKNTVSQ 537	ADASGSKNVYLKGIATTLTEPSAGAKSSHVD 866	425 LVNDFYNNGLPSNLSGGRNPSLDYGFKGGETAMASYCSELQFLANPVTNHVQSAEQHNQD 484	789 AKNLEVKTAKVSDTLTIGGNTPTGGTTATPKVNITSTADGLNFAKET- 835	366 TKMIEREINSVNDNPLIDVSRNKALHGGNFQGTPIGVSMDNTRLAIAAIGK-LMFAQFSE 424	731 INSAATFVKTENI/TTSIDEDNPTDNGKDDALKAGDTLTFKAGKNLKVKRDGKNITFDL 788	ILDGSDYVKAAQKVHEMDPLQKPKQDRYALKTSPQWLGPQIEVIRSS 365	687 VTKGGFETVKTGATUADKGKVTVKDATANDADKKVATVKDVATA 730

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Copyright (c) 1993 - 2003 Compugen Ltd.
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/cqn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution

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17,	بد ند	Sequence 36, App	Sequence 38, App	32,	Sequence 37, App.	35,		10	19,	Sequence 8, Appl	13,	48.	Sequence 47, App.	50,	49	5	Ņ	Sequence 1, Appli	Description	

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38,	Sequence 45, App	48,	47,	37,	Sequence 62, App	36,		Sequence 41, App	Sequence 65, Appl	Sequence 52, Ap	Sequence 12692, A	Sequence 5671, Ap	Sequence 53, Appl	Sequence 44, Appl	40,			Sequence 58, Appl				Sequence 12085, 🗚	Sequence 15, Ap	Sequence 30, Appl	

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; Patent No. US20020173633A1
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APPLICANT: Campos, Reinaldo
APPLICANT: No. US20020173633Alogaki, Hiroyuki
APPLICANT: No. US20020173633Alogaki, Hiroyuki
APPLICANT: Suslow, Trevor
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Characterization of Phenylalarine Andmonia Lyase (PAL)
TITLE OF INVENTION: Game in Wounded Lettuce Tissue
FILE REFERENCE: 023070-12450019
FILE REFERENCE: 023070-12450019
CURRENT APPLICATION NUMBER: US/09/964,992A
CURRENT FILING DATE: 2002-07-09
PRIOR APPLICATION NUMBER: US 60/245,956
PRIOR FILING DATE: 2002-09-26
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                          121 GALQKELIRFLNAGIFGNGTETSHTLPHSATPAAMIVRINTLLQGYSGIRFEILEAITKF 180
                                                                          1 MENGHHYNGYVNELCIKDFLNWGYAAEALTGSHLDEVKKMYAEFFKPYVKLGGETLTYSQ 60
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US-09-964-992A-2
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LENGTH: 713
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Suslow, Trevor
APPLICANT: The Regents of the University of California
APPLICANT: The Regents of the University of California
TITLE OF INVENTION. Characterization of Phenylaianine Ammonia-Lyase (PAL)
TITLE OF INVENTION: Gene in Wounded Lettuce Tissue
FILE REFERENCE: 023070-124500HS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Saltveit, Mikal E
APPLICANT: Campos, Reinaldo
APPLICANT: No. US20020173633Alogaki, Hiroyuki
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NUMBER OF SEQ ID NOS: 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 60/235,956
                                                                                                                                                                                                                      OTHER INFORMATION: lettuce phenylalanine ammonia-lyase (PAL) OTHER INFORMATION: (LSPAL2)
                                                                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                                              ORGANISM: Lactuca sativa
                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
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                                                                                                            Local Similarity
                            1 MENGNHVNGVVNELCIK-DPLNWGVAAEALTGSHLDEVKKMVAEERKPVVKLGGETLTVS 59
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US-09-964-992A-5
                                                                                                                                           SEQ ID NO 5
LENGTH: 666
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 5, Application US/09964992A Patent No. US20020173633A1
                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 60/235,956
PRIOR FILING DATE: 2000-09-26
NUMBER OF SEQ ID NOS: 13
                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: The Regents of the University of California TITLE OF INVENTION: Characterization of Phenylalanine Ammonia-Lyase (PAL) TITLE OF INVENTION: Gene in Wounded Lettuce Tissue FILE REFERENCE: 023070-124500US
                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/964,992A CURRENT FILING DATE: 2002-07-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Saltveit, Mikal E.
                                                                                                                                                                                                          SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                         OTHER INFORMATION: sunflower phenylalanine ammonia-lyase (PAL)
                                                            FEATURE:
                                                                               ORGANISM: Helianthus annuus
                                                                                                                        TYPE. PRT
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                                          SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 49
LENGTH: 717
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                                                                                                                                                                                                                                                                                                                                                 Sequence 49, Application US/09854122 Patent No. US20020016980A1
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                                                                                                                                                                                                                             APPLICANT: ALBERTE, RANDALL S.
APPLICANT: SMITH, ROBERT
TITLE OF INVENTION: TRANSFERIC PLANTS INCORPORATING TRAIT OF ZOSTERA MARINA
FILE REFERENCE: PHA-007.01
                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/854,122 CURRENT FILING DATE: 2001-09-10
                                                                                                                                      PRIOR APPLICATION NUMBER: 50/202,529 PRIOR FILING DATE 2000-05 10
                                                                                                                  NUMBER OF SEQ ID NOS: 51
ORGANISM: Arabidopsis thaliana
                           TYPE: PRT
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 50
LENGTH: 700
                                                                                                                                                                                                                                                                                                                                                                                           Sequence 50, Application US/09854122 Patent No. US20020016980A1
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                                                                                                              CURRENT APPLICATION NUMBER: US/09/854,122 CHERENT FILIN: CATE 2001-09-10 FFIOR APPLICATION NUMBER: 50/202,529 PRIOR FILING DATE 2000-05-10
                                                                                                                                                                                                                                             FILE REFERENCE: PHA-007.01
                                                                                                                                                                                                                                                                   APPLICANT: ALBERTE, RANDALL S.
APPLICANT: SMITH, ROBERT
TITLE OF INVENTION: TRANSGENIC PLANTS INCOMPORATING THAIT OF ZOSTEKA MAKINA
                                                                                              NUMBER OF SEQ ID NOS: 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         664 GRGFLTGEKVTSPGEEFDRVFTAMCKGGLIDPLLECLGGWNGEPLPIC 711
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US-09-854-122-47; Sequence 47, Application US/09854122; Patent No. US20020016980A1
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                         SEQ ID NO 47
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                                                                                                    TITLE OF INVENTION: TRANSGENIC PLANTS INCORPORATING TRAIT OF ZOSTERA MARINA FILE REFERENCE: PHA-007.01
CURRENT APPLICATION NUMBER: US/09/854,122
CURFENT FILING DATE 2001.09-10
PRIOR APPLICATION NUMBER: 60/202,529
PRIOR APPLICATION NUMBER: 60/202,529
PRIOR FILING DATE: 2000-05-10
                                                                     NUMBER OF SEQ ID NOS: 51
                                                  SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                   APPLICANT: ALBERTE, RANDALL S. APPLICANT: SMITH, ROBERT
LENGTH: 304
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                                                                                                                                                                                                                                                                SMITH, ROBERT
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US-09-854-122-48
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US-09-854-122-48
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LENGTH: 303
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Patent No. US20020016980A1
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PRIOR FILING DATE: 2000-05-10
NUMBER OF SEW ID NUS: 51
SOFTWARE: Patentin Ver. 2.1
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APPLICANT: SMITH, ROBERT
TITLE OF INVENTION: TRANSGENIC PLANTS INCOPPORATING TRAIT OF ZOSTERA MARINA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/854,122 CURRENT FILING DATE: 2001-09-10
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                                                    579 SGTYPLMQKLRQVLVDHALNNGETEKNTNTSIFQKIATFEBELKVLLPKEV 629
                                                                                                                  193 DLRHMEENLKASVKNTVSQVAKRVLTMTANGELHPSRFCEKDLLKVVDREYVFSYIDDFC
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253 SATYPLMQKLRSVLVDHALNNGDKEKDEAMSIFQKIAVFEEELIAVFPKEV 303
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                                                                                                                                                                                                                                                                                            SYCSELOFLANPVINHVQSAEQHNQDVNSLGLISARKTAEAVDILKLMSSTYLVALCQSI 518
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87.6%; Pred. No. 9.9e-95;
rative 20; Mismatches 16; Indels 0
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SEQ ID NO 13
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APPLICANT: Kootstra, Anna
TITLE OF INVENTION: Phenylalanine Ammonia Lyase Polypeptide and
TITLE OF INVENTION: Polynucleotide Sequences and Methods of Obtaining and
TITLE OF INVENTION: Using Same
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LOCATION: (153)
OTHER INFORMATION: Other information: Xaa - Val or Ala
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                      549 G-ELHESRECEKDILLKYVDKEY-----VFAYIDDVCSCIYPLMQKI.KQVI.VDHAI.NNGE 601
                                                                           513 ISARRTAEANDVLSLLLASHLYCTIQAVELRAMELDEKKQEDPLLPTLLQQHLGTGLDVN 572
                                                                                                                              491 ISARKTAEAVDILKLMSSTYLVALCQSIDLRHLEENMKSTVKNTVSQVAKKVLTMG--VN 548
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                                                                                                                                                                                      NRGLPSCLA-AEDPSLNYHGKGLDTHTAAYASELGHLANPVTTFVQPAEMGNQAVNSLAL 512
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482 GHLANPVTTHVQPAEMANQAVNSLALISAKRTTESNDVLSLILLATHLYCVLQALDI.RATE 541
                                                         465 QFLANPVTNHVQSAEQHNQDVNSLGLISARKTAEAVDILKLMSSTYLVALCQSIDLRHLE 524
                                                                                                                                                                              405 DNTRLAFAATGKLMFAQFSELVNDFYNNGLPSNLSGGRNPSLDYGFKGGETAMASYCSEL 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   185 LVVLEALTNFLNHGITPIVPLRGTISASGDLSPLSYIAAAISGHPDSKVHVVHEGKEKIL
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                                                                                                                                                                                                                                          363 YPLRTSPQWLGPLVSDLTHAHAVLTIEAGQSTTDNPLIDVENKTSHHGGNFQAAAVANTM 422
                                                                                                                                                                                                                                                                                                   346 YALRTSPQWLGPQ1-EVIRSSTKMIEREINSVNDNPLIDVSRNKALHGGNFQCTP1GVSM 404
                                                                                                                                                                                                                                                                                                                                                               303 AMVGHAGSFHPFLHDVTRPHPTQIEVAGNIRKLLEGSRFAVHHEEEVKVKDDEGILRQDR 362
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            171 FEILEALTKFLANNITPCLPLRCTITASGDLVPLSYTAGLLTGRPNSKA-VGPTG--EVI. 227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Match 27.3%, Score 994.5, UB 1 Local Similarity 35.9%, Pred. No. 3.2e-68;
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                                                                                                                     EKTRLGLAQIGKLNFTQLTEMLNAGMNRGLPSCLA-AEDPSLSYHCKGLDIAAAAYTSEL 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YAREAMALENLEP - - VVI.GPKEGLGLVNCTAVSASMATLALHDAHMLSLLSQSLTAMTVE
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                                                                                                                                                                                                                                                                                                                                                                                                                     VMQGKP-EFTDHLTHKLKHHPGQIEAAAIMEYILDGSDY-VKAAQKVHEMDPLQKPKQDR 345
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 09/624,693
PRIOR FILING DATE: 2000-07-24
PRIOR APPLICATION NUMBER: PCT/US01/23270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/939,408A CURRENT FILING DATE: 2001-08-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Phenylalanine Ammonia Lyase Polypeptide and TITLE OF INVENTION: Polynucleotide Sequences and Methods of ObTITLE OF INVENTION: Using Same FILE REFERENCE: 29479/500NSCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Yoshida, Roberta
APPLICANT: Kootstra, Anna
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR FILING DATE: 2001-07-24
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363 YPLRTSPQWLGPLVSDLIHAHAVLTIEAGQSTTDNPLIDVENKTSHHGGNFQAAAVANTM 422
                                                              346 YALRTSPOWLGPQI-EVIRSSTKMIEREINSVNDNPLIDVSRNKALHGGNFQGTPIGVSM 404
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                                                                                                                               303 AMVGHAGSFHPFLHDVTRPHPTQIEVAGNIRKLLEGSRFAVHHEEEVKVKDDEGILRQDR 362
                                                                                                                                                                                          288 VMQGKP-EFTDHLTHKLKHHPGQIEAAAIMEYILDGSDY-VKAAQKVHEMDPLQKPKQDR 345
                                                                                                                                                                                                                                                        245 YAREAMALENLEP--VVLGPKEGLGLVNGTAVSASMATLALHDAHMLSLLSQSLTAMTVE 302
                                                                                                                                                                                                                                                                                                                      228 NAEKAFAAAGVEGGFFELQPKEGLALVNGTAVGSGMASMVLFDANVLALLSEVLSAIFAE 287
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Local Similarity 35.9%; Pred No. 3.2e-68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                71 DV--VSAARKGRPVRVKDSDEIRSKIDKSVEFILRSQLSMSV--YGVTTGFGGSADTRTED 126
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SOFTWARE: Microsoft Office 97
SEQ ID NO 10
LENGTH: 716
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: BIOPRODUCTION OF PAKA-HYDROXYCINNAMIC ACID FILE REFERENCE: BC1009 US CIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Tang, Xiao-Song
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288 VMQGKP-EFTDHLTHKLKHHPGQIEAAAIMEYILDGSDY-VKAAQKVHEMDPLQKPKQDR 345
                                                             245 YAREAMALENLEP--VVLGPKEGLGLVNGTAVSASMATLALHDAHMLSLLSQSLTAMTVE 302
                                                                                                                                                                                                    185 LVVLEALTNFLNHGITPIVPLRGTISASGDLSPLSYIAAAISGHPDSKVHVVHEGKEKIL
                                                                                                                                                                                                                                                              171 FEILEAITKFLNNNITPCLPLRGTITASCDLVPLSYIAGLLTGRPNSKA-VGPTG--EVL 227
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                                                                                                                                  228 NAEKAFAAAGVEGGFFELQPKEGLALVNGTAVGSGMASMVLFDANVLALLSEVLSALFAE 287
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                                                                                                                                                                                                                                                                                                                                   AISLQKALLEHQLCGVLPSSFDSFRLGRGLENS--LPLEVVRGAMTIRVNSLTRGHSAVR 184
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US-09-765-873A-34
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                                                                                                                                                                                                                                                      : OTHER INFORMATION: x= Thr. Ala. Ser. Pro. Gly US-09-765-873A-34
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                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                       Matches 270;
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                                                                                                                                                                                                                                                                                                                                                 LOCATION: (138)..(138)
OTHER INFORMATION: x-leu, Met, ile, Val, Cys
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60 QVAGIAAANDSDTVKVELSEAARAGVKASSDWVMESMNKGTDSYGVTTGFGATSHRRTKQ 119
                                                 14 NGVAS---AKQAVNGASTNI.AVAGSHLÆTTÖVTÖVDI VEKMLAAPIDSILELDGYSI.NI.G 70
                                                                                                                                                                            Local Similarity
                                                                                                8 NGVVNELCIKDPLNWGVAAEALTGSHL-------DEVKKMVAEFRKPVVKLGGETLTVS 59
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                                                                                                                                                                    27.2%, Score 991.5, DB 10 35.9%; Pred. No. 5.5e-68;
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Sequence 35, Application US/09765873A
Patent No. US20010053847A1
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                                                                                                                                                                                                                      SOFTWARE: Microsoft Office 97 SEQ ID NO 35
                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 09/627,216 PRIOR FILING DATE 2000-07-27
                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 60/147,719 PRIOR FILING DATE: 1999-08-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Tang, Xiao-Song
TITLE OF INVENTION: BIOSPECIMETION OF PAPA-HYDROXYCINNAMIC
                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 38
                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/765,873A
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                 LOCATION: (198)..(198)
OTHER INFORMATION: X= Asp, Asn, Glu, Gln
                                                                                                                                       ORGANISM: mutant from Rhodotorula
                                                                                                                                                                    TYPE. PRT
NAME/KEY: UNSURE
                                                                               NAME/KEY: UNSURE
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; OTHER INFORMATION: X= Thr, Ala, Ser, Pro, Gly
US-09-765-873a-35
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US-09-765-873A-37
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                                                                                                                Sequence 37, Application US/09765873A
Patent No. US20010053847A1
GENERAL INFORMATION:
APPLICANT: Tang, Xiao-Song
TITLE OF INVENTION: BIOPRODUCTION OF PARA-HYDROXYCINNAMIC ACID
FILE REFERENCE: BC1009 US CIP
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CURRENT APPLICATION NUMBER: US/09/765,873A CURRENT FILING DATE: 2001-01-19 PRIOR APPLICATION NUMBER: US 09/627,216 PRIOR FILING DATE: 2000-07-27
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LOCATION: (540)...(540)
OTHER INFORMATION: X= Thr, Ala, Ser, Pro, Gly
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LOCATION. (202)...(202)
OTHER INFORMATION: x= Val, Met, Leu, Cys
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§69 TGEKVTSPGEEFDRVFTAMCKGQIIDPLLECL 700
                                                      625 WKVAAAESAISLTRQVRETFWSAASTSSPALSYLSPRTQILYAFVREELGVKARRGDVFL 684
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                                                                                                             -RIAYENDTLSIPNRIK-----ACRSYP------LYRFVREELG----RG--FL 668
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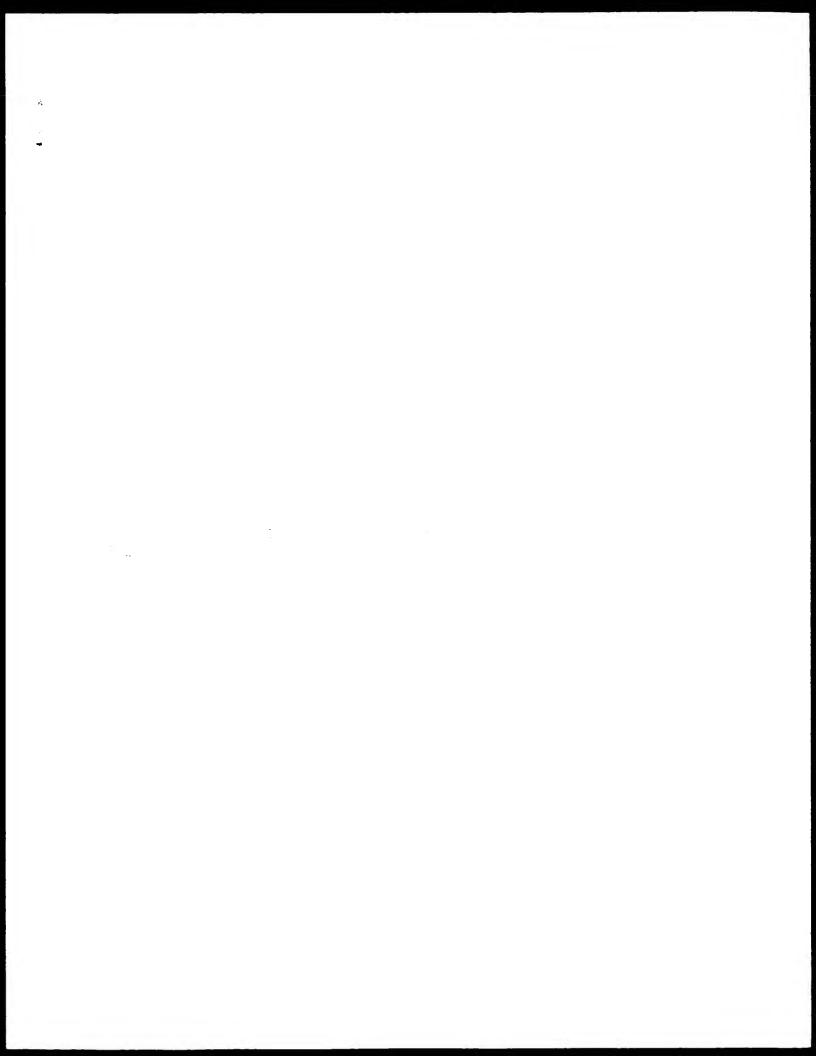
685 GKQEVTI-GSNVSKIYEAIKSGRINNVILKMI, 715

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: Sequence 32, Application US/09765873A

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PRIOR APPLICATION NUMBER: US 60/147,719
PRIOR FILING DATE: 1999-08-06
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PRIOR APPLICATION NUMBER: US 09/627,216
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555 LEQTNSYDLVPRWHDAFSFAAGTVVEVLSSTSLSLAAVNAWKVAAAESAISLTRQVRETF 614
                                                           605 NTNTSIFQKIATFEEELKVLLPKEVEGV----
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Local Similarity 36 2%; Pred No. 9.6e-68;
hes 265; Conservative 121; Mismatches 240; Indels 10;
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                                                                                                                                                                            MGVNGELHPSRECEKDLLRVVDREYVEAYIDDVCSGTYPLMQKLRQVLVDHALNNGETEK 604
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                                                           -----RIAYENDTLSIPNRIK--- 648
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SUMMARIES

716 2 S48 717 2 S56		11111111111111111111111111111111111111
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. 4 716 2 \$04.643 . 4 718 2 \$48725 . 0 708 2 \$14.2725 . 0 708 2 \$14.2725 . 0 708 2 \$13.633 . 4 715 2 \$66.643 . 712 2 \$103.663 . 5 715 2 \$102.665 . 713 2 \$102.665 . 713 2 \$102.665 . 713 2 \$102.665 . 714 2 \$102.665 . 715 2 \$102.665 . 716 2 \$102.665 . 717 2 \$102.666 . 717 2 \$102.666 . 718 2 \$52.603 . 718 2 \$52.603 . 718 2 \$52.603 . 718 2 \$52.603 . 718 2 \$52.603 . 718 2 \$52.603 . 718 2 \$52.603 . 718 2 \$52.603 . 718 2 \$52.603 . 718 2 \$52.603 . 718 2 \$52.603 . 718 2 \$52.603 . 718 2 \$52.603 . 718 2 \$52.603 . 718 2 \$52.603 . 718 2 \$56.645 . 718 2 \$56.645	77778888888888888888888888888888888888	
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. 4 716 2 S0463 . 4 718 2 S48725 . 0 708 2 T14275 . 0 708 2 T14295 . 1 715 2 S66343 . 5 715 2 J02565 . 712 2 T01858 . 5 710 2 J02565 . 713 2 S22603 . 723 2 S22603 . 723 2 S22603 . 724 2 S44133 . 725 2 S17444 . 725 2 S17446 . 727 2 S174672 . 74672	& & & & & & & & & & & & & & & & & & &	
. 4 716 2 S0463 .4 718 2 S48726 .0 4 718 2 S48726 .0 708 2 T14925 .4 715 2 S66343 .5 715 2 J02365 .7 719 2 T01858 .7 719 2 S25672 .7 719 2 S25672 .7 719 2 S25673 .7 721 2 S17444 .9 712 2 S17444 .9 712 2 S17444 .9 712 2 S17444 .9 712 2 S04127 .7 705 2 S17444 .9 712 2 S04127 .1 725 2 G84787	20000000000000000000000000000000000000	
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histidine ammonia	E82228	1 2	8 51	14.	540.5	5
phenylalanine ammo	501999	2		26.	971.5	4
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phenylalanine amm	S25538	5		£6.	474	1.
phonylalanine amm	N56628	5		27	994 5	=
phonylalanine ammo	T06546	19 2		37.	1368	ō
phenylalanine ammo	. JQ1070	6 2		51	1867	9
probable phenylal	T05968	7 2		51.	1887	38
phenylalanine ammo	705955	(i)		(S)	1948	7 7
phenylalanine amm	T05970	9 2	9 549	599	2184	36
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ALIGNMENTS

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Accession: f12749 Mazcytat, FA. Mazcytat, F. Maccession: T12749 Accession: T12749 Best Local sintlarity 94.4%: Pred. No. 1.4e-197 Best Local similarity 94.4%: Pred. No. 1.4e-197 Best Local similarity 94.4%: Pred. No. 1.4e-197 Accession: T12749 Accession: T12741 Accession: T12749 Accession: T12740 Accession: T12740 Accession: T12740 Accession: T12740 Accession: T12740 Accession: T12740 Accession:	RESULT 1 T12749 T12749 Phenylalanine ammonia-lyase (EC 4.3.1.5) - common sunflower C;Species: Helianthus annuus (common sunflower) C;Date: 13 Aug-1999 #sequence_revision 13 Aug-1999 #text_change 29-Jun-2000

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C:Keywords: ammonia-lyase; carbon-ohtrogen lyase
F:202-304/Cross-link: 5-inida:colinone (Ala-Gly) *status pred
F:203/Modified site: dehydroalanine (Scr) *status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        phenylalaninc ammonia-lyase (EC 4.3.1.5) - parsley
C:Species: Petroselinum crispum (parsley)
C:Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 21-May-1999
C:Accession: S04463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Qy
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A; Residues: 1 716 <LOI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R:Lois, R.; Dietrich, A.; Hahlbrock, K.; Schulz, W. EMBO J. 8, 1641-1648, 1989
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Title: A phenylalanine ammonia-lyase gene from parsley: structure, A;Reference number: S04463, MUID.89356635, PMID:2767049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Accession: S04463
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                                                                                                                                                                                                            233 FAAAGVEGGFFELQPKEGLALVNGTAVGSGMASMVLFDANVLALLSEVLSAIFAEVMQGK 292
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                     353 QWLGPQIEVIRSSTKMIEREINSVNDNPLIDVSKNKALHGGNFQGTPIGVSMDNTRIAIA 412
                                                                                                                                                                                                                                                                                                                                       173 ILEALTKFLNNNITPCLPLRGTITASGDLVPLSYTAGLL/TGRPNSKAVGPTGEVLNAFKA 232
                                                                                                                                                                                                                                                                                                                                                                                                                                              113 SHRRTKQGGALQKELIRFLNAGIFGNGTETSHTLPHSATRAAMIVRINTLLQGYSGIRFE 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     661 EELG 664
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 GETLTISQVAAT-SARDGSGVTVELSEAARAGVKASSDWVMDSMNKGTDSYGVTTGFGAT 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        53 GETLTVSQVAGIAAANDSDTVKVELSEAARAGVKASSDWVMESMNKGTDSYGVTTGFGAT 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MENGNGATTNGHVNGNGMDFCMKTEDPLYWGIAAEAMTGSHLDEVKKMVAEYRKPVVKLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MENGN-----HVNGVVNELCIK--DPLNWGVAAEALTGSHLDEVKKMVAEFRKPVVKLG 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
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                                                                         PEFTDHLTHKLKHHPGQIEAAAIMEHILDGSAYVKAAQKLHEMDPLQKPKQDRYALRTSP
                                                                                                                                                                                                                                                                                                                                                                                           SHRRTKQGGALQKELIRFLNAGIFGNGSD--NTLPHSATRAAMLVRINTLLQGYSGIRFE 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ETEKNANTSIFQKIATFEDELKAILPKEVESVRVAFENGTMSIPNRIKACRSYPLYRFVR 660
                                                                                                                                PEFTDHETHKLKHHPGQ1EAAAIMEY1LDGSDYVKAAQKVHEMDPLQKPKQDRYALRTSP 352
                                                                                                                                                                                   FKLAGVEGGFFELQPKEGLALVNGTAVGSGMASMYLFEANILAVLAEVMSAIFAEVMQGK
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                                                                                                                                                                                                                                                                                      ILEAITKFLNQNITPCLPLRGTTTASGDLVPLSY LAGLLTGRPNSKAVGPTGVILSPEEA
620;
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86.2%;
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Pred. No. 2.3e
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240

187 FLNHNITPCLPLRGTITASGDLVPLSYIAGLLTGRPNSKAVGPTGVTLSPEEAFKLAGVE

246

GALQKELIRFLNAGIFGSGAEAGNNTLPHSATRAAMLVRINTILQGYSGIRFEILEAITK 186
FLNNNITPCLPLRGTITASGDLVPLSYIAGLLTGRPNSKAVGPTGEVLNAEKAFAAAGVE 239

GGFFELQPKEGLALVNGTAVGSGMASMVLFDANVLALLSEVLSAIFAEVMQGKPEFTDHL 299

127

121 GALQKELIRFLNAGIFGMGTET-SHTLPHSATKAAMIVKINTLLGGGGGGFEILEAITK 179

VAAISARDDSG-VKVELSEEAPAGVKASSDWVMDSMNKGTDSYGVTTGFGATSHRPTKQG 126

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Title: Structural and catalytic properties of the four phenylalanine ammonia-lyase A; Reference number: S48725; MUID:95010141; PMID:7925471 A; Accession: S48726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      phenylalanine ammonia-lyase (EC 4.3.1.5) 3 - parsley
C:Species. Petroselinum crispum (parsley)
C:Date: 18-Oct.1995 #sequence_revision 12-Apr-1996 #text_change 16-Jul-1999
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A; Residues: 1-58, 'E', 60-718 <APP2>
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A; Residues: 1-718 <APP1>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references. EMBL.X81159; NID:g535007, PIDN:CAA57057.1; PID.g535008
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Cross-references: EMBL: X81159
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                                                                                                                                                                                                                                                                   Query Match
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J. Blochem. 225, 491–499, 1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   593 VDHALNNGETEKNTNTSIFQKIATFEEELKVLLPKEVEGVPIAYENDTLSIPNPIKACPS 652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              473
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61 VAGIAAANDSDTVKVELSEAARAGVKASSDWVMESMNKGTDSYGVTTGFGATSHRRTKQG 120
                                                                                                                                                                                                                                       Loca I
                                                                                                                                            3 NGNHVNGVVNELCIK--DPLNWGVAAEALTGSHLDEVKKMVAEFRKPVVKLGGETLTVSQ 60
                                                                                    NG-HANGNGLDLCMKKEDPLNWGVAAEALTGSHLDEVKRMVAEYRKPVVKLGGETLTISQ 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YPLYKFVRKELGTEYLTGEKVTSPGEEFEKVFIAMSKGEIIDPLLECLESWNGAPLPIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NTVSQVAKKVLTMGVNGELHPSRFCEKDLLRVVDREYVFAYIDDVCSGTYPLMQKLRQVL 592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NHVQSAEQHNQDVNSLGLISSRKTSEAVEILKLMSTTFLVGLCQAIDLRHLEENLKSTVK 537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NHVQSAEQHNQDVNSLGLISARKTAEAVDII.KLMSSTYLVALCQSIDI.RHI.EENMKSTVK 532
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                                                                                                                                                                                                           621;
                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                 87.4%;
87.2%;
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RESULT 4
S48725
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C:Keywords: ammonia lyase; carbon-nitrogen lyase
F:202-204/Cross-link: 5 imida:olinone (Ala-Gly) *status predicted
F:203/Modified site: dehydroalanine (Ser) *status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eur. J. Biochem. 225, 491-499, 1994.
A:Title: Structural and catalytic properties of the four phenylalanine ammonia-lyase iso
A:Reference number: S48725, MOID:95010141, PMID:7925471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R:Appert, C.: Logemann, E., Hahlbrock, K., Schmid, J., Amrhein, N
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A:Status: nucleic acid sequence not shown
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C:Species: Petroselinum crispum (parsley)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:X81159: NID-9534892; PIDN-CAA57056 1; PID:g534893
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A; Pesidues: 1:716 - APP -
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                                                  173 ILEAITKELNNNITPCLPLRGTITASGDLVPLSYIAGLLTGRPNSKAVGPTGEVLNAEKA 232
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                                                                                                                                                                                                                          61 GETUTISQVAA1-SARDGSGVTVELSEAARAGVKASSDWVMDSMNKGTDSYGVTTGFGAT 119
                                                                                                                                                                                                                                                                               53 GETLTVSQVAGIAAANDSDTVKVELSEAARAGVKASSDWVMESMNKGTDSYGVTTGFGAT 112
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                                                                                                                                                                                                                                                                                                                                           1 MENGNGAITNGHVNGNGMDFCMKTEDPLYWGIAAEAMTGSHLDEVKKMVAEYRKPVVKLG 60
                                                                                                                                                                                                                                                                                                                                                                                                 1 MENGN-----HVNGVVNELCIK--DPLNWGVAAEALTGSHLDEVKKMVAEFRKPVVKLG 52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REELGRGFITGEKVTSPGEEFDPVFTAMCKGQIIDPLLECLGGWNGEPLPIC 711
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                                                                                                                                                                 SHRRTKQGGALQKELIRFLNAGIFGNGTETSHTLPHSATRAAMIVRINTLLQGYSGIRFE 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GDKERNLSTSTFQKTAAFEDELKALLPKEVETARAALESGNPATPNRIKECRSYPLYKEV 666
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KRVLTMGVNGELHPSRFCEKDLLRVVDREYIFAYIDDPCSATYPLMQKLRETLVEHALNN
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ILEATTKELNQNITPCLPLRGTITASGDLVPLSYTAGLLTGRPNSKAVGPTGVILSPEEA 237
                                                                                                              SHRRTKQGGALQKELIRFLNAGIFGNGSD--NTLPHSATRAAMLVRINTLLQGYSGIRFE 177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             620;
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                                                                                                                                                                                                                                                                                                                                                                                              C;Keywords: ammonia-lyase; carbon-nitrogen lyase
F;194-196/Cross-link: 5-imidazolinone (Ala-Gly) *status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                 A, Pathway. phenylpropanoid metabolism C; Superfamily: histidine ammonia-lyase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R:Takeda, J.: Ozeki, Y.: Yoshida, K. Photochem. Photochem. Photochem. Photochem. Proceding for induction of promoter activity of phenylalanine ammonia A.Title: Action spectrum for induction of promoter activity of phenylalanine ammonia A.Reference number: Z17966, MIID-97478956; PMID:9337617
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C;Sate: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-3ul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  phenylalanine ammonia-lyase (FC 4.3.1.5) - carrot
C;Species. Daucus carota (carrot)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Introns: 126/2
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                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                             Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               478 NHVQSAEQHNQDVNSLGLISSRKTSEAVEILKLMSTTFLVGLCQAIDLRHLEENIKSTVK 537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  473 NHVQSAEQHNQDVNSLGLISARKTAEAVDILKLMSSTYLVALCQSIDLRHLDENMKSTVK 532
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  598 VEHALKNGDNERNMNTSIFQKIATFEDELKALLPKEVESARAALESGNPAIPNFIEECRS 657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        593 VDHALNNGETEKNTNTSTEGKTATEEEELKVILLPKEVEGVRTAYENDITLSTENRTKACES 652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             538 NTVSSVAKRVLIMGVNGELHPSRFCEKDLLRFVDREYTFAYTDDPCSATYPLMQKLRQTL 597
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            358 QWLGPQ1EVTRSSTKMTERETUSVNDUPLTDVSRUKATHGGUFGGTP1GMSMDNTRLATA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  353 QWLGPQTEVIRSSTKMIEPEINSVNDNPLITVSPNKALHGGNEGGTPIGVSMDNTPLAIA 412
                    62 VAATAAG----SVKVELAESARAGVKASSDWVMESMNKGTDSYGVTTGFGATSHRRTKQG
                                                                          61 VAGIAAANDSDTVKVELSEAARAGVKASSDWVMESMNKGTDSYGVTTGFGATSHERTKQG 120
                                                                                                                                                                                                                                                                                  Local
                                                                                                                                                              2 ENGNHVNGVVNELCI-KDPLNNGVAAFALTGSHLDEVKKMVAEFRKPVVKLGGEILTVSQ 60
                                                                                                                                4 ENKNYVIG--NGLCMQKDPLNWGMAAFAL/TGSHLDEVKRMVAEFRKPMVQLGGETL/TVSQ 61
                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                            87.0%;
87.2%;
                                                                                                                                                                                                                                            41;
                                                                                                                                                                                                                                                                               Pred. No. 2e-195
                                                                                                                                                                                                                                                                                                          Score 3171.5;
                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                       DB 2; Length 708;
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                                                                                                                                                                                                                                                     Indels
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C:Keywords: ammonia-lyase; carbon-nitroqen lyase
F:201-203/Cross-link: 5-imidazollnone (Ala-Gly) *status predicted
F:202/Modified site: dehydroalanine (Ser) *status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: DNA
A;Residues: 1-715 <FUK>
A;Cross-references: EMBL:M84466; NID:g170349; PIDN:AAA34122.1; PID:g170350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Title: Phenylalanine ammonia-lyase gene structure, expression, and evolution in Nicot A;Reference number: S66343; MUID:96194455; PMID:8624404 A;Accession: S66343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Fukasawa-Akada, T.
Rifukasawa-Akada, T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        phenylalanine ammonia-lyase (EC 4.3.1.5) 1 - common tobacco
C:Species: Nicotiana tabacum (common tobacco)
C:Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 16-Jul-1999
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                                                                                                                                                                                                                                                                                                                                                                                       A; Gene: PAL1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Status: preliminary
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                                                                                                                                                                                                                                                   202/Modified site: dehydroalanine (Ser) #status predicted
                                                                                                                                                        Matches
                                                                                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             541 KVLTMGVNGELHPSRFCEKDLLRVVDREYVFAYIDDVCSGTYPLMQKLRQVLVDHALNNG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            298
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  58
                                                                                                                                                                                Local Similarity
VSQVAGIAAANDS-DTVKVELSEAARAGVKASSDWVMESMNKGTDSYGVTTGFGATSHRR 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EELGTVYLTGEKVTSPGEEFDKVFTAMSKGEIIDPLLACLESWNGAPLPI 707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QFSELVNDFYNNGLPSNLSGGRNPSLDYGFKGGEIAMASYCSELQFLANPVTNHVQSAEQ 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GALQKELIRFLNAGIFGNGTETSHTLPHSATRAAMIVKINTLLQGYSGIRFEILEAITKF 180
                                                  MASNGHVNGGENFELCKKSADPLNWEMAAESLRGSHLDEVKKMVSEFRKPMVKLGGESLT 60
                                                                                                MENGNHVNGVVN-ELCIK--DPLNWGVAAEALIEGSHLDEVKKMVAEERKPVVKIGGETLI 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EELGRGFLTGEKVTSPGEEFDRVFTAMCKGQIIDPLLECLGGWNGEPLPI 710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ETEKNLSTSIFQKIAAFEDELKALLPKEVESARAVVESGNPAIPNRIKECRSYPLYKFIR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ETEKNTNTSIFOKIATFEEELKVLLPKEVEGVRIAYENDTLSIPNRIKACRSYPLYRFVR 660
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                                                                                                                                                        610;
                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     T.; Kung, S.; Watson, J.C.
30, 711-722, 1996
                                                                                                                                                                              85.3%;
                                                                                                                                                      45;
                                                                                                                                                                                                      Score 3149;
                                                                                                                                                                           Pred.
                                                                                                                                                      Mismatches
                                                                                                                                                                                No. 5.7e-194;
                                                                                                                                                                                                      DB 2;
                                                                                                                                                      56;
                                                                                                                                                                                                   Length 715;
                                                                                                                                                   Indels
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A; Title: Phenylalanine ammonia-lyase in tobacco. Molecular cloning and gene expressio A; Reference number: Z14995; MUID:95125127; PMID:7824656
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                                                                                                                                                                                                                                                                                                                         RFYREELGRGFLTGEKVTSPGEEFDRVFTAMCKGQIIDPLLECLGGWNGEPLPIC 711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PQIEVIRAATKMLEREINSVNDNPLIDVSRNKALHGGNFQGTPIGVSMDNARLALASIGK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RFVRKELGTELLTGEKVRSPGEECDKVFTAMCNGQIIDPMLECLKSWNGAPLPIC 715
                                                                                                                                                                                                                                                                                                                                                                                              MNNGESEKNVNSSIFQKIGAFEDELKAVLPKEVESAPAALESGNPAIPNRITECRSYPLY
                                                                                                                                                                                                                                                                                                                                                                                                                                          LNNGETEKNTNTSIFOKIATFEEELKVLLPKEVEGVRIAYENDTLSIPNRIKACRSYPLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QVAKRTLTMGANGELHPARFCEKELLRIVDREYLFAYADDPCSCNYPLMQKLRQVLVDHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QVAKKVLIMGVNGELHPSRFCEKDLLRVVDREYVFAYIDDVCSGTYPLMQKLRQVLVDHA 596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SAEQHNQDVNSLGLISARKTAEAVDILKLMSSTYLVALCQAIDLRHLEENLKNAVKNTVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SAEQHNQDVNSI.GLISARKTAEAVDILKIMSSTYLVAI.CQSIDLRHI.EENMKSTVKNTVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LMFAQFSELVNDYYNNGLFSNLTASKNPSLDYGFKGAEIAMASYCSELQFLANPVTNHVQ 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LMFAQFSELVNDFYNNGLPSNLSGGRNPSLDYGFKGGEIAMASYCSELQFLANPVTNHVQ 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PQIEVIRSSTKMIEREINSVNDNPLIDVSRNKALHGGNFQGTPIGVSMDNTRLAIAAIGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DHLTHKLKHHPGQIEAAAIMEHILDGSSYYKAAQKLHEMDPLQKPKQDRYALRTSPQWLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DHLTHKLKHHPGQTEAAATMEYTLDGSDYVKAAQKVHEMDPLQKPKQDRYALRTSPQWLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GVNGGFFELQPKEGLALVNGTAVGSGMASMVLFDSNILAVMSEVLSAIFAEVMNGKPEFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ITKLINSN1TPCLPLRGT1TASGDLVPLSYIAGLLTGRPNSKAVGPNGETLNAEEAFRVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ITKFLNNNITPCLPLRGTITASGDLVPLSYIAGLLTGRPNSKAVGPTGEVLNAEKAFAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TKQGGALQKELIRFLNAGIFGNGTETSHTLPHSATRAAMIVRINTLLQGYSGIRFEILEA 176
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                                                                                                                                                                                                                                                                                                                                                                                              660
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A;Description: catalyzes the deamination of L-phenylalanine to trans-cinnamic acid A;Note: strongly induced during the hypersensitive reaction to TMV or to a fungal cC;Superfamily: histidine ammonia-lyase C;Keywords: ammonia-lyase; carbon-nitrogen lyase C;Keywords: ammonia-lyase; carbon-nitrogen lyase F;198-200/Cross-link: 5-imidazolinone (Ala-Gly) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R,Pellegrini, L.; Rohfritsch, O.; Fritig, B.; Legrand, M. Plant Physiol. 106, 877-886, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     phenylalanine ammonia-lyase (EC 4.3.1.5) - common tobacco
C:Species: Nicotiana tabacum (common tobacco)
                                                                                                                F;199/Modified site: dehydroalanine (Ser) #status predicted
                                                                                                                                                                                                                                                                                                                                                            C; Function:
                                                                                                                                                                                                                                                                                                                                                                                                      A;Gene: PAL
                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references EMBL X78269; NID-y633596; PIDN CAA55075.1, PID y633597 A;EXperimental source: cultivar Samsun NN; tissue-type leaves after infection by toba
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-712 < PEL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Accession: T03663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C,Date: 24·Mar·1999 *sequence_revision 24-Mar-1999 *text_change 16-Jul-1999
C;Accession: T03663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 T03663
85.6%;
                                     Score 3118.5;
                                     DB 2;
                                 Length 712;
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Matches

602;

Conservative

38;

Pred. No. Mismatches

5.2e-192;

Indels

1.

Gaps

1.

eli

Local Similarity

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C:Superfamily hisibline ammonia-lyase
C:Keywords: ammonia-lyase; carbon-nitrogen lyase
F:201-203/Cross-link: 5 imidazolinone (Ala_Cly) #status_predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               phenylalanine ammonia lyase (EC 4.3.1.5) - western balsam poplar x cottonwood C:Species: Populus trichocarpa x Populus delicides (western balsam poplar x cottonwood) C:Date: 40-Sept1993 #sequence_revision 20-Aug 1994 #text_change 28-May-1999 C:Paccession: JQ2265
                                                                                                                                                                                                               A.Cross references: GB:L11747; NID:g169453; FIDN:AAA33805.1; FID:g169454
A:Note: the authors translated the codon AAG for residue 331 as GLu and AAG for residue C:Comment: The enzyme plays a role in linking primary metabolism to phenylpropanoid metabolism.
                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1-715 <SUB>
                                                                                                                                                                                                                                                                                                                                                                  A;Title: Structure, inheritance, and expression of hybrid popular (Populus trichocarpa A;Reference number: JQ2265; MUID:94151434, FMID.8108506 A;Accession: JQ2265
                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Subramaniam, R.; Reinold, S.; Molitor, E.K.; Douglas, C.J. Plant Physiol. 102, 71-83, 1993
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                                                                                                   F;202/Modified site: dehydroalanine (Ser) #status predicted
                        Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EINSVNDNPLIDVSRNKALHGGNEQGTPIGVSMDNARLALASIGKIMEAQESELVNDYYN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DECYKYDPLNWEMAADSLKGSHLDEVKKMYAEFRKPYYKLGGETLTYAQYAATAAKDNAK 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ELCIK-DPLNWGVAAEALTGSHLDEVKKMVAEFRKPVVKLGGETLTVSQVAGIAAANDSD 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KVRSPGEECDKVFTAMCNGQ1IDSLLECLKEWNGAPLPIC 712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QKILAFEGELKAVLPKEVESARISLENGNPAIANRIKECRSYPLYRFVREELGAELLTGE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SAPKTAEAVDILKLMSSTYLVALCQAIDLRHLEENLRNAVKNTVSQVAKRTLTMGANGEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NGLPSNLSGGRNPSLDYGFKGGEIAMASYCSELQFLANPYTNHVQSAEQHNQDVNSLGLI 491
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAAIMEYILLGSDYVKAAQKVHEMDPLQKPKQDKYALKTSPQWLGPQIEVIRSSTKMIER 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALVNGTAVGSGLASMVLFDANILAVFSEVLSAIFAEVMNGKPEFTDHLTHKLKHHPGQIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALVNGTAVGSGMASMVLFDANVLALLSEVLSAIFAEVMQGKPEFTDHLTHKLKHHPGQIE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TVKVELSEAARAGVKASSDWVMESMNKGTDSYGVTTGFGATSHPRTKOGGALQKELIRFL 131
                        85.5%;
84.1%;
Score 3116, Lp _,
No. 7.5e-192;
                                                Length, 715;
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ammonia-lyase

E-phenylalanine to trans cinnamic acid

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A,Description. cutal;2es
C;Superfamily: histidine
                                                                                                                                                C; Genetics:
                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-712 <T
                                                                                                                                                                                                                                                                                                                                     A; Accession: T01858
                                                                                                                                                                                                                                                                                                                                                                  A; Reference number: Z14446
                                                                                                                                                                                                                                                                                                                                                                                                                               R,Taguchi, G.; Sharan, M.; Gonda, K.; Yanagisawa, K.; Shimosaka, M.; Hayashida,
J. Plant Brochem. and Brotech. 7, 79-84, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Date: 26-Feb-1999 #sequence_revision 26-Feb-1999 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   phenylalanine ammonia-lyase (EC 4-3.1.5) - common tobacco
C.Species: Nicotiana tabacum (common tobacco)
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                                                             C; Function:
                                                                                      A; Introns: 130/2
                                                                                                                   A;Gene: palA
                                                                                                                                                                             A; Experimental source: strain Bright Yellow; tissue type callus
                                                                                                                                                                                                          A; Cross-references: EMBL: ABUU8199; PIDN: BAA22947.1
                                                                                                                                                                                                                                                                                                     A, Status: preliminary, translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                            A:Title: Effect of methyl jasmonate and elicitor on PAL gene expression in tobacco ou
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 599;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           664 REELGTVLLTGEKVQSPGEBEDKVFTAMCQGKIIDPMLECLGEWNGSPLPIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        604
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     660 REELGRGFLIGHKVTSPGHEFDRVFTAMCKGQTIDPLLECLGGWNGEPLPIC 711
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phenylalanine ammonia-lyase (EC 4.3.1.5) 1 - Lithospermum crythrorhizon C;Species: Lithospermum crythrorhizon C;Species: Lithospermum erythrorhizon C;Late: 09-Mar-1998 #sequence_revision 09-Mar-1998 #text_change 20-Jun-2000 C;Accession: JC5872; PC4506
R;Yazaki, K.; Kataoka, M.; Honda, G.; Severin, K.; Heide, L.
Biosci. Biotechnol. Biochem. 61, 1995-2003, 1997
A;Title. cDNA cloning and gene expression of phenylalanine ammonia-lyase in Lithospermum A;Reference number: JC5872, MUID 98101967; PMID:9438980
A;Accession: JC5872
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-710 <YAll>
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F:198-200/Cross-link, 5-imidazulinune (Ala Gly) #status predicted
F:199/Modified site: dehydroalanine (Ser) #status predicted
A;Residues: 1-710 <YA1>
A;Cross-references: DDBJ:D83075, NiD g2911121; Plbn:BAA24928 1; Plb:g2911122
A;Accession: PC4506
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86.1%; Pred. No. 1.9e-191;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               35; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            s of roots to protect them against pathogens in the soil C:Superfamily: histidine ammonia-lyase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: protein
A;Rusiducs: 348-479 \, YA2>
C;Comment: This enzyme catalyzes the first committed step in multibranched phenylprop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          밁
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     420 QFSELVNDYYNNGLPSNLTGSRNPSLDYGFKGAEIAMASYCSELQFLANPVTNHVQSAEQ
660 EELGTELLTGEKVRSPGEELDKVFTAMCEGKLVDPLLACLEAWNGAPLPIC
                                                                    661 EELGRGFLTGEKVTSPGEEFDRVFTAMCKGQIIDPLLECLGGWNGEPLPIC 711
                                                                                                                                                 600 ENEKDVNTSIFHKIAIFEEELKAILPKEVENARASVENGIPAISNRIEECRSYPLYKFVR
                                                                                                                                                                                                                                                                                          540 RTLTTGVNGELHPSRFSEKDLLRVVDREYVFAYADDPCLTTYPLMQKLRETLVGHALDNG
                                                                                                                                                                                                                                                                                                                                                                   541 KYLTMGVNGELHPSRFCEKDLLRVVDREYVFAYIDDVCSGTYPLMQKLRQVLVDHALNNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        361 VIRSSTKMIEREINSVNDNPLIDVSRNKALHGGNFQGTPIGVSMDNTRLAIAAIGKLMFA 420
                                                                                                                                                                                                                  601 ETEKNTNTSIFQKIATFEEELKVLLFKEVEGVKIAYENDTLSIFNKIKACKSYFLYKFYK
                                                                                                                                                                                                                                                                                                                                                                                                                                           480 HNQDVNSLGLISSRKTSEAVEILKLMSSSFLVALFQAVDLRHIEENVRLAVKNTVSQVAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         421 OFSELVNDFYNNGLESNISGGKNESLDYGEKGGELAMASYCSELOFLANPYTNHVQSAEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    301 HKLKHHEGQIEAAAIMEYILDGSDYVKAAQKVHEMDPLQKPKQDPYALRTSPQWLGPQIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            240 GFFELQPKEGLALVNGTAVGSGMASMVLYEANILAVLSEVISAIFAEVMNGKPEFTDHLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 GFFELQPKEGLALVNGTAVGSGMASMVLFDANVLALLSEVLSAIFAEVMQGKPEFTDHLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 I.NNNITPCLPIRGTITASGDLVPLSYIAGLLTGRPNSKAVGPTGEVLNAEKAFAAAGVEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               120 GALQKELIRFLNAGIFGNGTETSHTLPHSATRAAMLVRINTLLQGYSGIRFEILEAITKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 GALQKELIKFLNAGIFGNGTETSHTLPHSATRAAMIVRINTLLQGYSGIRFEILEAITKF 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 VAA1AARDDG--VTVELAEAAREGVKASSDWVMDSMNKGTDSYGVTTGFGATSHRRTKQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 VAGTAAANDSETVKVELSEAAPAGVKASSDWVMESMNKGTESVCVTTGPGATSHRRTKQC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 VENG---NGKTMEFCMKDPLNWEMASESMKGSHLDEVKNMVAEFRKPVVQLAGKTLT1GQ 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VIRSATKMIEREINSVNDNPLIDVSRNKALHGGNFQGTPIGVAMDNTRLAIASIGKLLFA
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83.5%; Pred. No. 2.2e-189;
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R;Kawamata, S.; Yamada, T.; Tanaka, Y.; Sriprasertsak, P.; Kato, H.; Ichinose, Y.; Plant Mol. Biol. 20, 167-170, 1992.
A;Title: Molecular cloning of phenylalanine ammonia-lyase cDNA from Pisum sativum. A;Keference number. S25303, MUID:92385763; PMID:1515609

phenylalanine ammonia-lyase (EC 4.3.1.5) - garden pea C:Species: Pisum sativum (garden pea) C:Eate: 93-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 20-Jun-2000

C; Accession: S25303

RESULT 11

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RESULT 12

$22991

phenylalanine ammonia-lyase (EC 4.3.1.5) 1 - soybean

C:Species: Glycine max (soybean)

C:Date: 06-Jan-1994 #sequence_revision 10-Nov-1995 #text_change 16-Jul-1999

C:Accession: $22991
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                                                A;Title. Sequence and structure of a phebylalarine ammonia-lyase gene from Giyeine max.
A;Reference number: $22991, MIII) 92190550, PMID:1799682
                                                                                                                                  R; Frank, B L.;
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A; Molecule type: DNA
                         A: Accession: S22991
                                                                                                     DNA Seq. 1, 335-346, 1991
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.Residues: 1·723 ∹KAW.
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;209-211/Cross-link: 5 imidamolinone (Ala-Gly) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                      663 LGRGFLTGEKVTSPGEEFDKVFTAMCKGQ1LDPLLECLGGWNGEPLP1 710
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     615 EKNLNTSIFQKIATFEDELKTLLPKEVESTRAAYESGNPTVPNKINGCRSYPLYRFVRQE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            196 NNVTPCL-LRGTTTASGDLVPLSYTAGLLTGRPNSKAHGTSGEILNAKEAFQSAETNDGF 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            183 NNITPCLPLRGTITASGDLVPLSYIAGLLTGRPNSKAVGPTGEVLNAEKAFAAAGVEGGF 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     123 LQKELIRFLNAGIFGNGTETSHTLPHSATRAAMIVRINTLLQGYSGIRFEILEAITKFIN 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63 GIAAANDSIYIYKVELSEAARAGVKASSDWVMESMNKGTDSYGVTTGFGATSHRRTKQGGA 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAKNNNMKVNS---ADPLNWGVAAEAMKGSHLDEVKRMVEEYRKPVVRLGGETLTLISQVA 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LTTGVNGELHPSRECEKDLLRVVDREHVFAYIDDPCSATYPLMQKLRQVLVDHALVNGES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QDVNSLGLISARKTAHAVDIIKIMSSTYLVALCQSIDLRHLEENMKSTVKNTVSQVAKKV 542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RSSTKMIEREINSVNDNPLIDVSRNKALHGGNFQGTPIGVSMDNTRLAIAAIGKLMFAQF 422
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LTMGVNGELHPSRFCEKDLLRVVDREYVFAYIDDVCSGTYPLMQKLRQVLVDHALNNGET 602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QDVNSLGLISSRKTYEAIEILQLMSSTFLIALCQAVDLRHLEENLKNSVKNIVSQVAKRT 554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SELVNDFYNNGLPSNLSASRNPSLDYGFKGSEIAMASYCSELQYLANPVTTHVQSAEQHN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESTKSTEREINSVNDNPLIDVSRNKALHGGNEQGTFIGVSMDNTRLALASIGKLLEAQE 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LKHHPGQIEAAAIMEHILDGSAYVKAAKKLHEMDPLQKPKQDRYALRTSPQWLGPLIEVI 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FELQPKEGLALVNGTAVGSGLASIVLFEANILAVLSEVLSAIFAEVMQGKPEFTDHLTHK
                                                                                                                                  Vodkin,
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83.9%;
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C:Accession: A44133; S51076 R:Lee, S.W.; Robb, J.; Nazar, R.N. J. Hiol Them 267, 11824-11839, 1

A; Title: Truncated phenylalanine ammonia-lyase expression A; Reference number: A44133; MUID:92291052; PMID:1601854

11

tomato (Lycopersicon

SA

1992

phenylalanine ammonia-lyase (EC 4.3.1.5) - tomato C:Species Lyropersicon esculentum (tomato) C:Date: 10 Mar 1994 #sequence_revision to Mar 1994

10 Mar 1994

#text_change

22

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C:KEywords ammonia lyase, carbon-nitrogen lyase
E;199-201/Cross-link: 5-imidazolinone (Ala-Gly) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A:Cross references: EMBL X52953; NID glx376; FIDN (AA37129.1; PID:q18377 C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      174
                                                 654 PLYKEVKELIGRGELIGEKVTSPGEEFLEVFTAMCKGQTTDP1LL513GGWNGEPLPT 710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               354 WIGPQIEVIRSSTKMIEREINSVNDNPLIDVSRNKALHGGNFQGTPIGVSMUNTRLAIAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            234 AAAGVEGGFFELQPKEGLALVNGTAVGSGMASMVLFDANVLALLSEVLSAIFAEVMQGKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MENGN-HVNGVVNELCI-----KDPLNWGVAAEALTGSHLDEVKKMVAEERKPVVKLGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DHALVNAECEKDVNSSIEQKIAIEEEELKNILPKEVEGARAAYESGKAAIPNKIQECRSY 655
                                                                                                                                                           DHALNNGETEKNTNTSIFQKIATFEEELKVLLPKEVEGVRIAYENDTLSIPNRIKACRSY 65
                                                                                                                                                                                                               TVSQVSKRILTTGVNGELHPSRFCEKDLLKVVDREYIFSYIDDFCSATYPLMQKLRQVLV 595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ELASINSEFFELQFKEGLALVNGTAVGSGLASMVLFEANTLAVLSEVLSATFAEVMOGKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HRRTKQGGALQKELIRFLNAGIFGNGTESSHTLPHTATFAAMLVFINTLLGGYSGIRFEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HRRTKOGGALQKELIRFLNAGIFGNGTETSHTLPHSATRAAMIVRINTLLOGYSGIRFEI
PLYKFVREELGTGLLTGEKVKSPGEEFDKLFTAMCQGKIIDPLMECLGEWNGAPLPI 712
                                                                                                                                                                                                                                                                                                                HVQSAEQHNQDVNSLGLISSRKTNEAIEILKLMSSTFLIALCQAIDLRHLEENLKNSVKN
                                                                                                                                                                                                                                                                                                                                                                     HVQSAEQHNQDVNSLGLISARKTAEAVDILKLMSSTYLVALCQSIDLRHLEENMKSTVKN 533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WEGPLIEVIRESTKSTEREINSVNUNPLIDVSKNKALHGGNF QGIF IGVSMUN I KLALAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EFTDHLTHKLKHHPGQIEAAAIMEHILDGSSYMKAAKKLHEIDPLQKPKQDRYALRTSPQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEATINGHONG----SECLSTAKGNNDPLNWGAAAEAMKGSHLDEVKRMVAEYRKPVVKLGG
                                                                                                                                                                                                                                                              TVSQVAKKVLTMGVNGELHPSRFCEKDIL RVVDREYVFAY I DDVCSGTYPLMGKL RQVLV 593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IGKEMFAQFSEEVNDFYNNGEPSNESGGRNPSEDYGFKGGEIAMASYCSEEQFEANPVTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LEAITKILNNNVTPCLDLRGTITASGDLVPLSYIAGILTGRPNSKAVGPSGEVLNAKEAF
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A; Molecule type: DNA
A; Residues: 1-139 <LEW>
C; Genetics:
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C:Superfamily: histidine ammonia-lyase
C:Keywords: ammonia-lyase; carbon-nitrogen lyase
F:207-209/Cross-link: 5-imidazolinone (Ala-Gly) #status predicted
F:208/Modified site: dehydroalanine (Ser) #status predicted
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Eur. J. Blochem. 226, 109-114, 1994

A:Title: Differential utilization of alternate initiation sites in a plant defense gene A:Reference number: S51076; MUID:95045578; PMID:7957237

A:Accession: S51076
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-721 <LEE>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            355 LGPQ1EVIRSSTKMIEREINSVNDNPLIDVSRNKALHGGNFQGTP1GVSMDNTRLAIAA1 414
665 LYRLARQEAGLETTGEKARSDGEETDKALTALCUGOTIDDITECTKSMUGABIDIC
                                                      655 LYRFVREELGRGFLTGEKVTSPGEEFDRVFTAMCKGQIIDPLLECLGGWNGEPLPIC 711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            245 VAGVTSGFFELQPKEGLALVNGTAVGSGMASMYLFESNILAVMSEVLSAIFAEVMNGKPF 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                115 RRTKQGGALQKELIRFLNAGIFGNGTETSHTLPHSATRAAMIVRINTLLQGYSGIRFEIL 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65 LTVAQVASIANVDNKSNGVKVELSESARAGVKASSDWVMDSMGKGTDSYGVTTGFGATSH 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            56 LTVSQVAGIA-AANDSDTVKVELSEAARAGVKASSDWVMESMNKGTDSYGVTTGFGATSH 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MENGNHVNGVVNELC-----IKDPLNWGVAAEALTGSHLDEVKKMVAEFRKPVVKLGGET 55
                                                                                                                                                                                                                                                                                                                                                                              VQSAEQHNQDVNSLGLISARKTAEAVDILKLMSSTYLVALCQSIDLRHLEENMKSTVKNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GKLMFAQFSELVNDYYNNGLPLNLTAGRNPSLDYGLKGAEIAMASYCSELQFLANPVTNH
                                                                                                                                                                     HALNNGETEKNTNTSIFOKIATFERELKVLLPKEVEGVRIAYENDTLSIPNRIKACRSYP 654
                                                                                                                                                                                                                                 VSQVAKKTLAMGANGELHPARFCEKELLQVVEREYLFTYADDPCSSTYFLMQKLRQVLVD 604
                                                                                                                                                                                                                                                                                          VSQVAKKVLIMGVNGELHPSRFCEKDLLRVVDREYVFAYIDDVCSGTYPLMQKLRQVLVD 594
                                                                                                                                                                                                                                                                                                                                                   VQSAEQHNQDVNSEGLISARKTAEAVDILKLMSSTYLVALCQALDLRHLEENLKNAVKNT 544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GKLMFAQFSELVNDFYNNGLPSNLSGGRNPSLDYGFKGGEIAMASYCSELQFLANPVTNH 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FTDHLTHKLKHHPGQIEAAAIMEYILDGSDYVKAAQKVHEMDPLQKPKQDRYALRTSPQW 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAGVEGGFFELQPKEGLALVNGTAVGSGMASMVLFDANVLALLSEVLSAIFAEVMQGKPE 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EAITKLINSNITPCLPLRGTITASGDLVPLSYIAGLLTGRPNSKAVGPNGEKLNAEERFR 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EAITKFLNNNITPCLPLRGTITASGDLVPLSYIAGLLTGRPNSKAVGPTGEVINAEKAFA 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RRTKNGGALQKELIRFLNAGVFGNGTESSHTLPHSATRAAMLVRINTLLQGYSGIRFEIL 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VQNG-HVNGEAMDLCKKSINVNDPLNWEMAAESLRGSHLDEVKKMVDEFRKPIVFLGGET 64
                                                                                                                  HAMKNGESEKNLNSSIFQKIVAFEDELKAVLPKEVESARAVVESGNPAIPNRITECRSYP 664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LGPQIEVIRAATKMIEREINSVNDNPLIDVSRNKALHGGNFQGTPIGVSMDNTRLALASI
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83 0%; Pred No 9.8;
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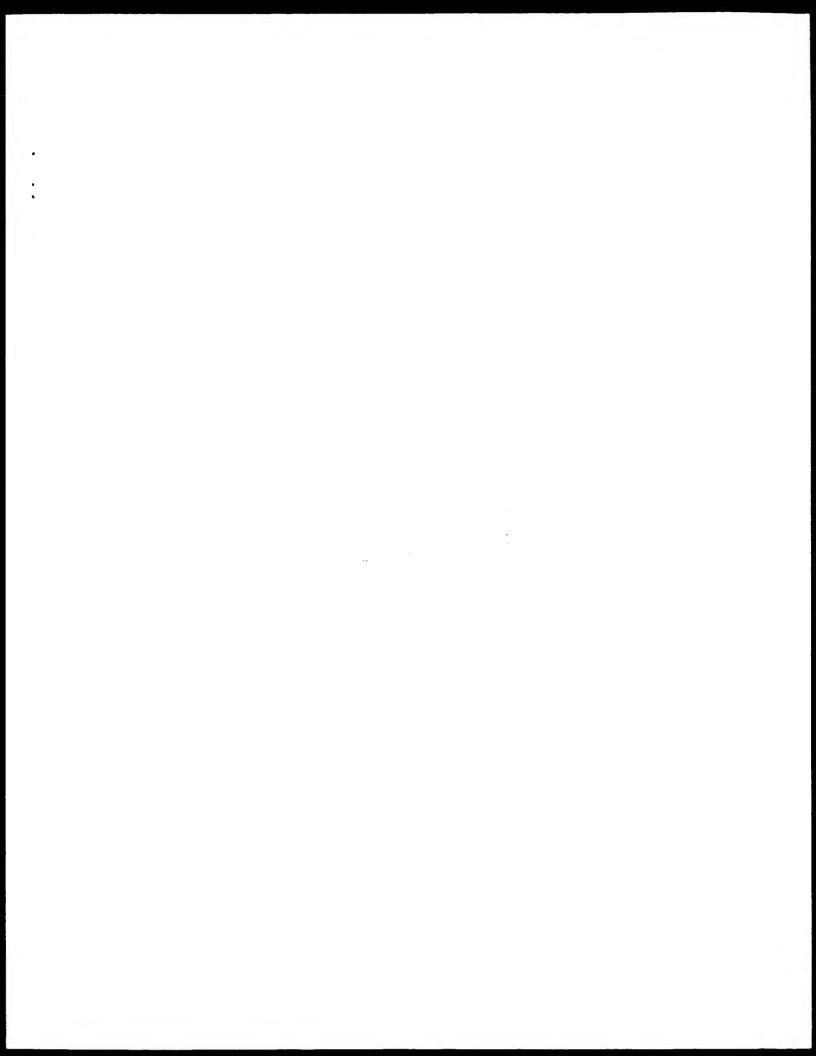
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C;Superfamily: histidine ammonia-lyase
C;Superfamily: histidine ammonia-lyase
C;Keywords: ammonia-lyase; carbon-nitrogen lyase
F;211-213/Cross-link: 5-imida.olinone (Ala-Gly) #status predicted
F;212/Modified site: dehydroalanine (Ser) #status predicted
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Plant Mol. Biol. 17, 415-429, 1991
A;Title: Stress responses in alfalfa (Medicago sativa L.). 12. Sequence analysis of p
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A; Residues: 1-725 <GOW>
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A;Accession: $17444
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665 RGFLTGEKVTSPGEEFDRVFTAMCKGQIIDPLLECLGGWNGEPLPIC 711
                                                                                              619 NFNTSIFOKIATFEEELKTLLPKEVESARTAYESGNPTIPNKINGCRSYPLYKFVREELG
                                                                                                                                                                                             605 NTNTSIFQKIATFEEELKVLLPKEVEGVRIAYENDTLSIPNRIKACRSYPLYRFVREELG 664
                                                                                                                                                                                                                                                                                                 559 MGVNGELHPSRFCEKDLLKVVDREHVFAYIDDPCSATYPLSQKLRQVLVDHALVNGESEK 618
                                                                                                                                                                                                                                                                                                                                                                                                    545 MGVNGELHPSRFCEKDLLRVVDREYVFAYIDDVCSGTYPLMQKLRQVLVDHALNNGETEK 604
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       485 VNSLGLISARKTAHAVDILKLMSSTYLVALCQSIDLRHLEENMKSTVKNTVSQVAKKVLT 544
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   185 ITPCLPLRGTITASGDLVPLSYIAGLLTGRPNSKAVGPTGEVLNAEKAFAAAGVEGGFFE 244
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Pred. No. 9.9e-189;
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phenylalanine ammonia-lyase (EC 4.3.1.5) class II - kidney bean C:Species: Phaseolus vulgaris (kidney bean) C:Botto. 28:Feb 1990 #sequence_revision 28:Feb-1990 #text_change 21-May-1999 C:Accession: S04127 C.Accession: S04127 K:Cramer, C.E.: Edwards, K. Dron, M.: Hang, X., Filling, S.E.; Rolwell, G. Plant Mol. Biol. 12, 367-383, 1989
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S04127
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C:Keywords: ammonia-lyase; carbon nitrogen lyase
F:198-200/Cross-link: 5 imidazolinone (Ala-Cly) #status predicted
F:199/Modified site: dehydroalanine (Ser) #status predicted
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619 EEELKTLLPKEVEGARLAYENDQCAIPNKIKDCKSYPLYKFVREELGTSLLTGEKVISPG 678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       378
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18 DPLNWGVAAEALTGSHLDEVKKMVAEFRKPVVKLGGETLTVSQVAGIAAANDSDTVKVEL 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Match 83.9%; Score 3058; DB 2; Local Similarity 84.3%; Pred. No. 3.9e-188;
                           EMELKVLLPKEVEGVRIAYENDYLSIPNRIKACRSYPLYREVREELGRGFLTGEKVTSPG 677
                                                                                                                                                                                                                                                                                                                                       1.SGGRNPS1.DYGFKGGETAMASYCSELQFT.ANPYTNHVQSAFQHNQDVNSI.GI.ISARKTA 497
                                                                                                                                                                                                                                                                                                                                                                                                                                              | DNPLIDVSRNKALHGGNFyGTF1GVSMDNTKLAIAA1GKLMFAQFSELVNDFYNNGLPSN 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEAARAGVKASSDWVMESMNKGTDSYGVTTGFGATSHRRTKQGGALQKELIRFLNAGIFG 137
                                                                                                                                                                                                         EALETEKLMSSTFLVALCQATDERHLEENEKNTVKNVVSQVAKRTETTGVNGELHPSRFC
                                                                                                                                                                                                                                                             EAVDILKLMSSTYLVALCQSIDLRHLEENMKSTVKNTVSQVAKKVLTMGVNGELHPSRFC 557
                                                                                                                                                                                                                                                                                                                                                                                                                DNPLISVSRNKALHGGNFOGTPIGVSMENTRLAIASIGKLMFAQFSDLVNDYYNNGLPSN 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HILDGSSYIKAAKKLHEIDPLOKPKODRYALRTSPOWLGPOIEVIRFSTKSIEREINSVN 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AVGSGMASMVLFDANVLALLSEVLSALFAEVMQGKPEFTDHLTHKLKHHPGQIEAAAIME 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SGDLVPLSYTAGLLTGRPNSKAVGPTGEVLNAEKAFAAAGVEGGFFELQPKEGLALVNGT 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AESARACVKAISDWVMESMDKGTDSYGITTGFGATSHRRTKQGGALQKELIRFLNAGIFG 138
                                                                                                  EKALLKYVEREYTFAYIDDPCSGTYPLMQKLEQYLVDYALANGENEKNLNTSIFQKIASF 618
                                                                                                                                                        EKDLLRVVDREYVFAYIDDVCSGTYPLMQKLRQVLVDHALNNGETEKNTNTSIFQKIATF 617
                                                                                                                                                                                                                                                                                                              LTASRNPSLDYGFKGAEIAMASYCSELQYLANPVTSHVQSAEQHNQDVNSLGLISSRKTN 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SGDLVPLSYIAGLLTGRPNSKAVGPSGEILNAKEAFELANIGSEFFELQPKEGLALVNGT 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NGTESNCTLPHTATRAAMLYRVNTLLQGYSGIRFELLEAITKILNNNITPCLPLRGTITA 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   585; Conservative
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- Ş 678 EEFDRVFTAMCKGQIIDPLLECLGGWNGEPLPIC 711 679 EECDKVFSAMCQGKIIDPLLECLGEWNGAPLPIC 712

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Search completed: March 29, Job time: 51 secs 2003, 02:13:15



Scoring table: Title: Perfect score: OM protein - protein search, using sw model BLOSUM62 March 29, 2003, 00:34:05; Search time 39 Seconds (without aliquments) 756:145 Million cell updates/sec US-09-964-992A-1 3644 Gapop 10.0 , Gapext 0.5 1 MENGNHVNGVVNELCIKDPL Concore version 5.1 4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd. TIDPLIEGEGENGEPLPIC 711

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Total number of hits satistying chosen parameters:

112892 seqs, 41476328 residues

Post-processing: Minimum Match 0%

Maximum Match 100% Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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vuery Match
Best Local Similarity 94.4%; Pred. No. 1.4e-191;
Matches 627; Conservative 13; Mismatches 24; Indels 0; Gaps

0

1 MENGNHVNGVVNELCIKDPLNWGVAAEALTGSHLDEVKKMVAEFRKPVVKLGGETLTVSQ 60

2908.5 79.8 682 1 PALI POPKI 2908.5 79.8 70.3 1 PALY_MHENT 2730.5 74.9 70.0 1 FALY_WHENT 2672.5 73.3 62.0 1 PALY_PERAE 2632.5 73.2 71.0 1 PAL3_PHAVU 2585.5 71.0 695 1 PAL3_PHAVI 2585.5 71.0 695 1 PAL3_PHAVI 2585.5 71.0 695 1 PAL4_PPAVI 2586.6 70.1 PAL4_PPAVI 2586.6 70.1 PAL4_PPAVI 2586.6 70.1 PAL4_PAVI 2586.6 70.1 PAL4_PPAVI 2586.6 70.	79.8 682 PALL POPKI 79.8 703 PALY WHEAT 74.9 700 PALY WHEAT 73.3 620 PALY WHEAT 73.2 710 PALZ DRYSA 71.1 710 PAL3 PHAVU 71.0 695 PAL3 PHAVU 71.0 695 PAL3 PANTH 694 570 PAL3 PANTH 695 PAL4 POPKI 696 701 PAL4 DRYSA 69.6 701 PAL4 DRYSA					25							34 29
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	P45731 942504 943210 943221 75457227 719143 719143 74143 940912 940912 952777 752718	PALI PHAVU	PALY_PINTA	PAL1_ORYSA	PAL4_POPKI	PAI 2_SOI TH	PAL3_ARATH	PAL3_PHAVU	PAL2_ORYSA	PALY_PERAE	PALY_WHEAT	PALY_BROF1	PALT_POPKI

ALIGNMENTS

RESULT 1
PALY_HELAN

Lyase; Phenyipropanoid metabolism; Multigene lamily. SITE 197 199 MÜDETELE TO FORM 4-METHYLIDENE-IMIDAZOLE: 5-ONE (BY SIMILARITY)	FT SI
FROSITE, PS00488; PAL HISTIDASE; 1.	
pfam, pr00221; pAL; 1.	
HSSP; P21310; 188F.	
EMBL, Y12461, CAA73065.1,	
or send an email of incenseers sip.on).	
tities requires a license agreement (See http://www.isb-sib.ch/a	
modified and this statement is not removed. Usage by and for commercial	oc mo
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WHICH IS FORMED AUTOCATALYTICALLY BY CYCLIZATION AND DEHYDRATION OF RESIDNES ALA-SER-CIV (BY SIMILARITY)	J C
 PATHWAY: Phenylpropanoid biosynthesis; first step. 	<u>.</u> .
FIRST REACTION IN THE RIOSYNTHESIS FROM L-PHENYLALANINE OF A WIDE	음:
-!- FUNCTION: THIS IS A KEY ENZYME OF PLANT METABOLISM CATALYZING THE	
(In) Plant Gene Register PGR98-108.	
Tourvielle D., Ledoigt C.;	RA TO
Mazeyrat F.A., Salles S., Drevet T., Rheckel-Drevet P.,	
SEQUENCE FROM N.A.	
MORT Tay (n=4000)	2 2
Asteridae; euasterids II; Asterales; Asteraceae; Asteroideae;	
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;	
karyota; Viridiplantae; Streptophýta; Embryophyta; Tracheophyta;	
lianthus annuus (Common sunflower).	OS He
enylalanine ammonia-lyase (EC 4.3.1.5).	
15-JUN-2002 (Rel. 41, Last annotation update)	
15-JUL-1998 (Rel. 36, Last sequence update)	
1998	
PALY HELAN STANDARD: PRT: 667 AA	ID PALY

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                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trachec Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids II; Apiales; Apiaceae; Petroselinum.
                                                                                                                                                                                                                                                                                                                 01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Phenylalanine ammonia-lyase 1 (EC 4.3.1.5).
                                                           EMBO
                                                                                                          Lois R., Dietrich A., Hahlbrock K., Schulz W.; "A phenylalanine ammonia-lyase gene from parsley: structure.
                      SEQUENCE FROM N.A.
                                                                        cis-acting elements."
                                                                                             regulation and identification of elicitor and light responsive
                                                                                                                                                MEDLINE=89356635; PubMed=2767049;
                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                             Petroselinum crispum (Parsley) (Petroselinum hortense)
                                                                                                                                                                                                        NCBI_TaxID=4043;
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                                                           J. 8:1641-1648(1989).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ETEKNANTSIFQKIATFEDELKAILPKEVESVRVAFENGTMSIPNRIKACRSYPLYRFVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KVLTMGVNGELHPSRFCEKDLLRVVDREYVFAYIDDVCSGTYPLMQKLRQVLVDHALNNG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HNQDVNSLGLISARKTAEAVDILKLMSSTYLVALCQSIDLRHLEENMKSTVKNTVSQVAK 540
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Logemann E.,
                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
     Hahlbrock
                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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                                                                                                                                                                                                                                                        Tracheophyta;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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"Serine-202 is the putative precursor of the active site dehydroalanine of phenylalanine ammonia lyase. Site-directed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lyase; Phenylpropanoid metabolism; Multigene family.

SITE 202 204 MODIFIED TO FORM 4-METHYLIDENE-IMIDAZOLE-
SITE 5-OME (BY SIMILARITY).

MUTAGEN 203 203 S->A: COMPLETE LOSS OF ACTIVITY.

MUTAGEN 210 210 S->A: NO LOSS OF ACTIVITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TIGREAMS; TIGKUIZZZ, L
DROSITE; PS00488; PAL_HISTIDASE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001106; Phe/His_NH3lyase
Pfam; PF00221; PAL; 1.
TIGRFAMs; TIGR01226; phe_am_lyase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; S04463; S04463.
HSSP; P21310; 1B8F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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SUBCELLULAR LOCATION: Cytoplasmic (Probable).
PTM: CONTAINS AN ACTIVE SITE 4-METHYLIDENE-IMIDAZOLE-5-ONE (MIO). WHICH IS CONTAINS AN ACTIVE SITE 4-METHYLIDENE-IMIDAZOLE-5-ONE (MIO). WHICH IS CONTAINS AN ACTIVE SITE 4-METHYLIDENE-IMIDAZOLE-5-ONE (MIO). OF RESIDNES ALA-SEP-GLY (BY SIMILAPITY)
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PEFTDHLTHKLKHHPGQIEAAAIMEHILDGSAYVKAAQKLHEMDPLQKPKQDRYALRTSP
                                                                                                                                                                                                                                                                                                                                     GETLTISQVAAI-SARDGSGVTVELSEAARAGVKASSDWVMDSMNKGTDSYGVTTGFGAT
                                         PEFTDHLTHKLKHHPGQIEAAAIMEYILDGSDYVKAAQKVHEMDPLQKPKQDRYALRTSP
                                                                                  FKLAGVEGGFFELQPKEGLALVNGTAVGSGMASMVLFEANILAVLAEVMSAIFAEVMQGK
                                                                                                                         FAAAGVEGGFFELQPKEGLALVNGTAVGSGMASMVLFDANVLALLSEVLSAIFAEVMQGK 292
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                                                                                                                                                                                                                                                   SHRRTKQGGALQKELIRFLNAGIFGNGSD--NTLPHSATRAAMLVRINTLLQGYSGIRFE
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77828 MW;
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RESULT 3
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                                                                                                                                                                                                                                    the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for example
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Appert C., Logemann E., Hahlbrock K., Schmid J., Amrhein N.; "Structural and catalytic properties of the four phenylalanine ammonia-lyase isoenzymes from parsley (Petroselinum crispum Nyr Eur J Biochem 225:491-499(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota: Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; cudicotyledons; core eudicots;
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Petroselinum crispum (Parsley) (Petroselinum hortense).
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01-NOV-1995 (Rel. 32, Last Sequence update)
15-JUN-2002 (Rel. 41, Last amoutation update)
Phenylalanine ammonia-lyase 2 (EC 4.3.1.5).
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Lyase, Phenylpropanoid metabolism, SITE 202 204 MONTE
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                                      TIGREAMS; TIGRO1226; phe_am_lyase; prosite; psno488; pal_HISTIDASE; 1
                                                                                 InterPro; IPR001106; Phe/His_NH31yase
Plam; PF00221; PAL; 1.
                                                                                                                              EMBL; X81158, CAA57056.1;
HSSP; P21310; 188F.
                                                                                                                                                                                           or send an email to license@isb-sib.ch).
                                                                                                                                                                                                               entities requires a license agreement (See http://www
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SUBCELLULAR LOCATION: Cytoplasmic (Probable)
PTM: CONTAINS AN ACTIVE SITE 4-METHYLLOENE IMIDAZOLE-5-ONE
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PAL3_PETCR
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01-Nov-1995 (Rei. 32, Inst Sequence update)
15-NiN-2002 (Rei 41, Inst annovation update)
Phenylalanine ammonia-lyase 3 (EC 4.3.1.5).
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Spermatophyta: Magnoliophyta; eudicotyledons; core eudicots
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FKLAGVEGGFFELQPKEGLALVNGTAVGSGMASMVLFEANTLAVLAEVMSATFAEVMOGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FAAAGVEGGFFELQPKEGLALVNGTAVGSGMASMVLFDANVLALLSEVLSATFAEVMOGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ILEATTKELNNNITPCLPLRGTTTASGDLVPLSYTAGLLTGRPNSKAVGPTGEVLNAEKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SHKKTKQGGALQKELIKFINAGIFGNGSD--NILPHSAIKAAMIZKINILLQGYSGIRFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SHRRTKQGGALQKELTRFLNAGTFGNGTETSHTLPHSATRAAMIVRINTLLQGGSGIRFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GETLIFTSQVAAT-SARDGSGVTVELSEAARAGVKASSDWVMDSMNKGTDSYGVTTGFGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GETETVSOVAGIAAANDSDIVKVEESEAAKAGVKASSDWVMESMNKGIDSYGVIIGFGAT 112
                                                                                                                                                                                                                                                                                                                                                                                                                   YPLYKFVRKELGIEYLTGEKVTSPGEEFDKVFIAMSKGETIDPLLECLESWNGAPLPIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NTVSSVAKPVLTMGVNGELHPSRFCEKDLLRFVDREYIFAYIDDPCSATYPLMQKLFQTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A LOKEMPAQUESEL VNUEYNNG LESNESGORNESLUYCH KOAETAMASYCSEL QELANDVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PEFTDHLTHKLKHHM:QIEANAIMEYILC::SCYVKAAQKVHEMDFLGFFKGDPYALFTSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VEHALKNODNERNMNTS (FOR LATEFDELKALLPKEVESARAALESGNDALDNR LEECKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NTVSQVAKKVLTMGVNGELHPSRFCEKULLKVVDKEYVFAY I DDVCSGTYPLMQKLKQVL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   77964 MW; F7407HD881HEEE66 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 87.4%; Score 3185.5;
86.2%; Fred No. 2 K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                45;
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                                                                                                                            Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11; Caps
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MEDLINE-95010141; PubMed-7925471

SEQUENCE FROM N.A. NCBI_TaxID=4043;

euasterids II; Apiales; Apiaceae; Petroselinum

STINE REPRESENTATION OF THE PROPERTY OF THE PR

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PROSTIE; PS00488; PAL_HISTIDASE; 1.

Lyase; Phenylpropanoid metabolism; Multigene family.

Lyase; Phenylpropanoid metabolism; Multigene family.

SITE

MODIFIED TO FORM 4-METHYLIDENE-IMIDAZOLE-

SONE (BY SIMILARITY).
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-!- FUNCTION: THIS IS A KEY ENZYME OF PLANT METABOLISM CATALYZING THE FIRST REACTION IN THE BIOSYNTHESIS FROM L-PHENYLALANINE OF A WIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the FMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch)
    487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001106; Phe/His_NH31yase
                                                                                     480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
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CATALYTIC ACTIVITY: L-phenylalanine = trans-cinnamate + NH(3).
PATHWAY: Phenylpropanoid biosynthesis; first step.
SUBCELLULAR LOCATION: Cytoplasmic (Probable).
PTM: CONTAINS AN ACTIVE SITE 4-METHYLIDENE-IMIDAZOLE-5-ONE (MIO),
WHICH IS FORMED AUTOCATALYTICALLY BY CYCLIZATION AND DEHYDRATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: BELONGS TO THE PAL / HISTIDASE FAMILY.
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QHNQDVNSLGLISSRKTSEAVEILKLMSTTFLVGLCQAIDLRHLEENLKSTVKNTVSQVA 546
                                                                            QHNQDVNSLGLISARKTAEAVDILKLMSSTYLVALCQSIDLRHLEENMKSTVKNTVSQVA 539
                                                                                                                                                                                                                                                                                                                            EVIRSSTKM1EREINSVNDNPLIDVSRNKAIHGGNFQGSPIGVSMDNTRLAIAAIGKLMF 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      THKLKHHPGQIEAAAIMEYILDGSDYVKAAQKVHEMDPLQKPKQDRYALRTSPQWLGPQI 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGFFELQPKEGLALVNGTAVGSGMASMVLFDANVLALLSEVLSAIFAEVMQGKPEFTDHL 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GALQKELIRFLNAGIFGSGAEAGNNTLPHSATRAAMLVRINTLLQGYSGIRFEILEAITK 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GALQKELIRFLNAGIFGNGTET-SHTLPHSATRAAMIVRINTLLQGYSGIRFEILEAITK 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VAGIAAANDSDTVKVELSEAARAGVKASSDWVMESMNKGTDSYGVTTGFGATSHRRTKQG 120
                                                                                                                                                              AQFSELVNDFYNNGLPSNLSGGRNPSLDYGFKGAEIAMASYCSELQFLANPVTNHVQSAE
                                                                                                                                                                                                                                               AQFSELVNDFYNNGLPSNLSGGRNPSLDYGFKGGEIAMASYCSELQFLANPVTNHVQSAE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              THKLKHHPGQIEAAAIMEHILDGSAYVKAAQKLHEMDPLQKPKQDRYALRTSPQWLGPQI 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGFFELQPKEGLALVNGTAVGSGMASMVLFEANILAVLAEVMSAIFAEVMQGKPEFTDHL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           620;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             87.2%; Score 3178.5;
87.1%; Pred. No. 7.7
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      Matches
                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 l_DAUCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Takeda J., Ozeki Y., Yoshida K.;

"Action spectrum for induction of promoter activity of phenylalanine ammonia-lyase gene by UV in carrot suspension cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      023865;
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Phenylalanine ammonia-lyase 1 (EC 4.3.1.5).
                                                                                     SEQUENCE
                                                                                                                                                             TIGRFAMS; TIGR01226; phe_am_lyase; 1. PROSITE; PS00488; PAL_HISTIDASE; 1.
                                                                                                                                                                                                                                          EMBL; D85850; BAA23367.1; -. HSSP; P21310; 1B8F.
                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                            Lyase; Phenylpropanoid metabolism; Multigene family SITE 194 196 MODIFIED TO FORM 4-MET
                                                                                                                                                                                                                                                                                                    or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (See http://www.isb-sib.ch/announce,
                                                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-97478956;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=cv. Kurodagosun;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Daucus carota (Carrot)
                                                                                                                                                                                                       Pfam; PF00221; PAL; 1
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                                                                                                                                                                                                                           nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           667
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   547 KRVLTMGVNGELHPSRFCEKDLLRVVDREYIFAYIDDPCSATYPLMQKLRETLVEHALNN
                          Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CATALYTIC ACTIVITY: L-phenylalanine = trans-cinnamate + NH(3).
PATHMAY: Phenylpropanoid biosynthesis; first step.
SUBCELLULAR LOCATION: Cytoplasic (Probablet step.
PTM: CONTALMS AN ACTIVE SITE 4-METHYLIDEME-IMIDAZOLE-5-ONE (MIO).
WHICH IS FORMED AUTOCATALYTICALLY BY CYCLIZATION AND DEHYDRATION
OF RESIDUES ALA-SER-GLY (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: THIS IS A KEY ENZYME OF PLANT METABOLISM CATALYZING THE FIRST REACTION IN THE BIOSYNTHESIS FROM L-PHENYLALANINE OF A WILL VARIETY OF NATURAL PRODUCTS BASED ON THE PHENYLPROPANE SKELETON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: BELONGS TO THE PAL / HISTIDASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REELGTEYLTGEKVRSPGEEFEKVFTAMSKGEIIDPLLECLESWNGAPLPIC 718
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                      Similarity
                                                                                                                                                                                                                       IPR001106; Phe/His_NH31yase
                                                                                  708 AA;
    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PubMed-9337617;
                    87.0%;
87.2%;
                                                                                  76845 MW;
  41;
                  Pred.
                                         Score 3171.5;
                                                                                5-ONE (BY SIMILARITY).; 0610411373E680E3 CRC64;
                                                                                                                        MODIFIED TO FORM 4-METHYLIDENE-IMIDAZOLE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
    Mismatches
                      No. 2e-189;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            708 AA
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                                         DB 1; Length 708;
                                                                                                                                                                                                                                                                                                                                         Usage
    Indels
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RESULT PARKULT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              B
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P45726;
                                                                                                                                                                         "Molecular cloning of phenylaianine ammonia-lyase cDNA and classification of varieties and cultivars of tea plants (Camellia sinensis) using the tea PAL cDNA probe.";
Theor Appl. Genet 89 671-675(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ol-NOV-1995 (Rel. 32, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Phenylalanine ammonia-lyase (EC 4.3.1.5).
                                                                                                                                                                                                                                                                                                               STRAIN-CV. Ya
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta, Tracheo
Spermatophyta, Magnoliophyta; eudicotyledons; core eudicots;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Camellia sinensis (Tea)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1995
                                    -1- FUNCTION: THIS IS A KEY ENZYME OF PLANT METABOLISM CATALYZING TH FIRST REACTION IN THE BIOSYNTHESIS FROM L-PHENYLALANINE OF A WID VARLETY OF NATURAL PRODUCTS MASED ON THE PHENYLPPOPAME SKELETON.
-1- CATALYTIC ACTIVITY: L-phenylalanine - Lrans-cinnamale + NH(3).
                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Asteridae; Ericales; Theaceae; Camellia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           658
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PATHWAY: Phenylpropanoid biosynthesis; first step
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-1- PTM: CONTAINS AN ACTIVE SITE 4-METHYLIDENE-IMIDAZOLE-5-ONE (MIO).
WHICH IS FORMED AUTOCATALYTICALLY BY CYCLIZATION AND DEHYDRATION
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SIMILARITY: BELONGS TO THE PAL / HISTIDASE FAMILY.
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EKNLSTSTFQKTRAFEEEIKTLLPKEVESTRAAIENGNSAIPNRIKECRSYPLYKFVREE
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Best Local
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PROSITE: PS00488; PAL_HISTIDASE: Multigene family.

Lyase: Phenylpropanoid metabolism; Multigene family.

MODIFIED TO FORM 4-METH
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5-ONE (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PALI_TOBAC STANDARD; PRT; 715 AA P25872; 01-MAY-1992 (Rcl. 22, Created) 01-MAY-1992 (Rel. 22, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update)
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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SUBCELLULAR LOCATION: Cytoplasmic (Probable).
PTM: CONTAINS AN ACTIVE SITE 4-METHYLIDENE-IMIDAZOLE-5-ONE (MIO)
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                                                                                                VAQVAATAVRDKSANGVKVELSEEARAGVKASSDWVMDSMNKGTDSYGVFTGFGATSHRR 120
                                                                                                                                                                                           VSQVAGIAAANDS-DTVKVELSEAARAGVKASSDWVMESMNKGTDSYGVTTGFGATSHRR 116
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TKQGGALQKELIFFLNAGIFGNGTETSHTLPHSATRAAMIVFINTLLQGYSG1FFEILEA 176
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                                                                       RESULT 8
PAL3_TOBAC P45733;
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                                                                                                                                                                                                                                                                                 LNNGETEKNTNTSIFQKIATFEEELKVLLPKEVEGVRIAYENDTLSIPNRIKACRSYPLY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TKNGGALQKELIRFLNAGVEGNGTETSHTLPHSATRAAMLVRINTLLQGYSGIRFEILEA
                                                                                                                                          REVRKELGTELLTGEKVRSPGEECDKVFTAMCNGQIIDPMLECLKSWNGAPLPIC
                                                                                                                                                                                       REVREELGRGFLTGEKVTSPGEEFDRVFTAMOKGQIIDPLLEGGWNGEPLPIG 711
                                                                                                                                                                                                                                    MNNGESEKNVNSSIFQKIGAFEDELKAVLPKEVESARAALESGNPAIPNRITECRSYPLY
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                                                                                                                                                                                                                                                                                                                                                                          QVAKKVLTMGVNGELHPSRFCEKDLLRVVDREYVFAYIDDVCSGTYPI,MQKI,RQVI,VDHA
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                        PRT;
                        712 AA
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01-NOY-1995 (Rel. 32, Created)
01-NOY-1995 (Rel. 32, Last Sequence update)
15-UN-2002 (Rel. 41, Last annotation update)
Phenylalanine ammonia-lyase (EC 4.3.1.5).
                                                                                                                                                                                                   expression during the hypersensitive reaction to tobacco mosaic virus and the response to a fungal elicitor."; plant physiol. 106:897-886(1994).
-i- FUNCTION: THIS IS A KEY ENZYME OF PLANT METABOLISM CATALYZING THE FIRST REACTION IN THE BIOSYNTHESIS FROM L-PHENYLALANINE OF A WIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta, Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids 1; Solanales; Solanaceae; Nicotiana.
                                                                                                                                                                                                                                                                                                                                                                   STRAIN=cv. Samsun NN; TISSUE=Leaf; MEDLINE=95125127; PubMed=7824656;
                                                                                                                                                                                                                                                                                                                     Peilegrini L., Rohfritsch O., Fritig B., Legrand M.; "Pehenylalanine ammonia-lyase in tobacco. Molecular cloning and gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nicotiana tabacum (Common tobacco)
                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=4097;
                                                                                    VARIFTY OF NATURAL PRODUCTS BASED ON THE PHENYLPROPANE SKELETON. CATALITYTC ACTIVITY. L-phenylalanine - trans-cinnamate + NH(3). PATHWAY: Phenylpropanoid blosynthesis; first step. SUBCELLULAR LOCATION: Cyroplasmic (Probable). INDUCTION: STRONGLY INDUCED DURING THE HYPERSENSITIVE REACTION TO
                   TMV OR TO A FUNGAL ELICITOR.

PTM: CONTAINS AN ACTIVE SITE 4-METHYLLDENE-IMIDAZOLE-5-ONE (MIO)
WHICH IS FURMED AUTOCATALYTICALLY BY CYCLIZATION AND DEHYDRATION
OF RESIDUES ALA-SER-GLY (BY SIMILARITY)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tyase, Phenylpropanoid metabolism, Multigene family.

SITE 198 200 MODIFIED TO FORM 4-METHYLIDENE-IMIDAZOLE-
5-ONE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TIGREAMS; TIGRO1226; phc_am_lyase; 1. PROSITE; PS00488; PAL_HISTIDASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X78269; CAA55075.1;
HSSP; P21310; IB8F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00221; PAL; 1
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673 KVRSPGEECDKVFTAMCNGQIIDSLLECLKEWNGAPLPIC 712
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      73 TVKVELSEGARAGVKASSDWVMDSMSKGTDSYGVTTGFGAISHKKTKNGGALQKELIRFL 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     72 TVKVELSEAARAGVKASSIWVMESMNKGTDSYGVTTGGGATSHRRTKQGGALQKELIRFL 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13 DFCVKVDPLNWEMAADSLKGSHLDEVKKMVAEFRKPVVKLGGETLTVAQVAAIAAKDNAK 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13 ELCIK-DPLNWGVAAEALTGSHLDEVKKMVAEFRKPVVKLGGETLTVSQVAGIAAANDSD 71
                                                                                                                                                                                                                       HPSRFCEKULLRVVDREYVFAYIDDVCSGTYPLMQKLRQVLVDHALNNGETEKNTNTSIF ×11
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                                                                                     QKILAFEGELKAVLPKEVESARISLENGNPAIANPIKEGPSYPLYRFVPEELGAELLTGE 672
                                                                                                                             QKIATFEEELKVLLPKEVEGVRIAYENDTLSIPNRIKACRSYPLYRFVREELGRGFLTGE 671
                                                                                                                                                                             HPSRECEXULLRYVUREYVERYADDAGSANYFLMQKLKQVLVLHALENGENEKNANGSIF SILV
                                                                                                                                                                                                                                                                    SARKTAEAVDILKLMSSTYLVALCQAIDLRHLEENLRNAVKNTVSQVAKRTLTMGANGEL 552
                                                                                                                                                                                                                                                                                                             SARKTAEAVDILKIMSSTYLVALCQSIDIRHIEENMKSTVKNTVSQVAKKVIIMGVNGEL 55
                                                                                                                                                                                                                                                                                                                                                          NGEPSNETAGKNESEDYGEKGSEIAMASYCSELQFLANEVINHVQSAEQHNQDVNSLGLI 492
                                                                                                                                                                                                                                                                                                                                                                                                  NGLPSNLSGGRNPSLDYGFKGGEIAMASYCSELQFLANPVTNHVQSAEQHNQDVNSLGLI 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EINSVNDNFLIDVSRNKALHGGNFQGTPIGVSMDNTRLAIAAIGKLMFAQFSELVNDFYN 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAAIMEHILDGSSYVKAPQKLHETDPLQKFKQDRYALRTSPQWLGPQIEVIRSATKMIEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALVNGTAVGSGLASMVLFDANILAVESEVLSAIFAEVMNGKPEFTDHLTHKLKHHPGQIE 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RGTITASGDLVPLSYIAGLLTGRPNSKAVGPTGEVLNAEKAFAAAGVEGGFFELQPKEGL 251
                                        KVTSPGEEEDRVETAMCKGQ1IDPLLECLGGWNGEPLPIC 711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RCTITASCDLVPLSY1AGLLTGRPNSKAIGPNGETLNAEEAFRVAGVNSGFFELQPKEGL 252
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PALY_POPTR STAN
P45730;
P1-NOV-11995 (Rel. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        trichocarpa x Populus deltoides) phenylalanine ammonia-lyase genes.";
Plant Physiol. 102:71-83(1993).
PIRST REACTION IN THE BIOSYNTHESIS FROM L-PHENYLALANINE OF A WIDE VARIETY OF NATHRAL PROPENTS RASED ON THE PHENYLAPOPANE SKELETON.
PLANTAPIC ACTIVITY: L-phenylalanine - trans-cinnamate + NH(3).
PLANTAPIC ACTIVITY: L-phenylalanine - trans-cinnamate + NH(3).
PRH-WAY: Phenylpropanoid biosynthesis; first step.
PRH-ONTAINS AN ACTIVE SITE 4-METHYLDENE-IMIDAZOLE-5 ONE (MIO).
WHICH IS FERMED AUTOCATALTICALLY BY CYCLIZATION AND DEHYDRATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Viridiplantae, Streptophyta, Embryophyta; Tracheophyta; Spermatophyta: Magnoliophyta; eudicotyledons; core eudicots; Rosid eurosids I; Malpighiales; Salicaceae; Populus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1995 (Rel. 32, Last sequence update)
15-THN-2002 (Rel. 41, Last annotation update)
Phenylalanine ammonia-lyase (RC 4.3.1.5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-P.trichocarpa X P.delloides; TISSUE-Lea1; MEDLINE-94151434; PubMed-8108506;
                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TIGHFAMS; TIGH01226; phe_am_lyase; 1. PROSITE; PS00488; PAL_HISTIDASE; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; L11747; AAA33805.1; -
HSSP; F21310; 1B8F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS PROJECTTY is copyright It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Subramaniam R , Reinold S , Molitor E K , Douglas C.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lyase; Phenylpropanoid metabolism; Multigene tamily SITE 201 203 MoDIFIED TO FORM 4-MET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00221; PAL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (See http://www.isb/sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Populus trichocarpa (Western balsam poplar)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute. There are no restrictions on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Structure, inheritance, and expression of hybrid poplar (Populus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          interPro;
184 LLNNNITPCLPLRGTITASGDLVPLSYIAGLLTGPPNSKATGPTGEVLDAAEAFKAAGIE
                                                                                                           120 GGALQKELIFFLNAGIFGNGTETSHTLPHSATFAAMIVRINTLLQGYSGIRFEILEAITK 179
                                           180 FENNNLLPCLPLKGTLFASGDLVPLSYTAGLLTGRPNSKAVGPTGEVLNAEKAFAAAGVE 239
                                                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                               60 QVAGIAAANDSDTVKVELSEAAPAGVKASSDWVMESMNKGTDSYGVTTGFGATSHPPTKQ 119
                                                                                                                                                                        65 QVAST-AGHDTGDVKVELSESARPGVKASSDWVMDSMDKGTDSYGVTTGFGATSHRRTKQ
                                                                                                                                                                                                                                                           6 KNG-YQNGSLESLAVNQPDPLSWGVAAEAMKGSHLDEVKPMVADYRKPVVKLGGETLTIA 64
                                                                                                                                                                                                                                                                                                    2 ENGNHVNGVVNELCI - - KUPLNWGVAAEALIGSHLDEVKKMVAEEKKPVVNLGGETLTVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OF RESIDUES ALA-SER-GLY (BY SIMILARITY).
SIMILARITY: BELONGS TO THE PAL / HISTIDASE FAMILY.
                                                                                    GGALQKELIFFLNAGIFGNGTETCHTLPHSATRAAMLVRINTLLQGYSGIFFEILEAITR
                                                                                                                                                                                                                                                                                                                                                 599;
                                                                                                                                                                                                                                                                                                                                                                      h 85.5%; Score 3116;
Similarity 84 1%; Pred. No. 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IPR001106; Phe/His_NH3lyase.
                                                                                                                                                                                                                                                                                                                                                                                                                                      715 AA;
                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ب
                                                                                                                                                                                                                                                                                                                                                                                                                                    77918 MW;
                                                                                                                                                                                                                                                                                                                                               56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      MODIFIED TO FORM 4-METHYLIDENE-IMIDAZOLE-5-ONE (HY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                 Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                      589E837A6E8AF2H6 CRC64;
                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            715 AA
                                                                                                                                                                                                                                                                                                                                                                    5.8e-186;
                                                                                                                                                                                                                                                                                                                                                                                           DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Usage
                                                                                                                                                                                                                                                                                                                                                                                        Length 715;
                                                                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 10
                                          use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.ish-sib-ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                            "A full-length cDNA for phenylalanine ammonia-lyase cloned from ripe Sweet Cherry fruit (Prunus avium).";
(In) Plant Gene Register PGR98-184.
-i- FUNCTION: THIS IS A KEY ENZYME OF PLANT METABOLISM CATALYZING THE FIRST REACTION IN THE BIOSYNTHESIS FROM L-PHENYLALANINE OF A WIDE VARIETY OF NATURAL PRODUCTS BASED ON THE PHENYLAROPANE SKELETON.
-i- CATALYTIC ACTIVITY: L-phenylalanine - trans-cinnamate + NH(3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidericots; Rosaceae; Amygdaloideae; Prunus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PAL.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PALL_PRUAV STANDARD; PRT; 717 AA. 064963; 30-MAY-2000 (Rel. 39, Created) 30-MAY-2000 (Rel. 39, Last sequence update) 15-JIN-2002 (Rel. 41, Last annotation update) Phenylalanine ammonia-lyase 1 (EC 4.3.1.5).
                                                                                                                                                                                   This
                      or send an email to license@isb-sib.ch)
                                                                                                                              the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-CV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Prunus avium (Cherry)
                                                                                                                                                          between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wiersma P.A., Wu Z.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=42229;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                244 SGFFELQPKEGLALVNGTAVGSGLASMVLFETNVLAVLSELLSAIFAEVMNGKPEFTDHL
                                                                                                                                                                                                                                                                                                           PATHWAY: Phenylpropanoid biosynthesis; first step.
SUBCELLULAR LOCATION: Cytoplasmic (Probable).
PTM: CONTAINS AN ACTIVE SITE 4-METHYLLDENE-IMIDAZOLE-5-ONE (MIO)
                                                                                                                                                                                                                                  OF RESIDUES ALA-SER-GLY (BY SIMILARITY). SIMILARITY: BELONGS TO THE PAL / HISTIDASE FAMILY.
                                                                                                                        SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                        WHICH IS FORMED AUTOCATALYTICALLY BY CYCLIZATION AND DEHYDRATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REELGTVLLTGEKVOSPGEEFDKVFTAMCQGKIIDPMLECLGEWNGSPLPIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  THKLKHHPGQIEAAAIMEYILDGSDYVKAAQKVHEMDPLQKPKQDRYALRTSPQWLGPQI 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REELGRGFLTGEKVTSPGEEFDKVFTAMCKGQIIDPLLECLGGWNGEPLPIC 711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GETEKNTNTSIFQKIATFEEEELKVLLPKEVEGVRIAYENDTLSIPNRIKACRSYPLYRFV 659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KRVLTTGANGELHPSRFCEKELLKVVDREYVFAYVDDPCSATYPLMQKLRQVFVDHALEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QHNQDVNSLGLISSRKTAEAVDII.KLMSTTFLVALCQAIDI.RHLEENLKSAVKNTVSQVS 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QHNQDVNSLGLISARKTAEAVDILKLMSSTYLVALCUSIDLRHLEENMKSTVKNTVSQVA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCFFFLQPKECLALVNCTAVCSCMASMVLFDANVLALLSEVLSAIFAEVMQCKPFFTDHL 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENEKNFSTSVFQKIEAFEEELKALLPKEVESARAAYDSGNSAIDNKIKECRSYPLYKFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KKYLTMGYNGELHPSRFCEKDLLRYYDREYYFAYIDDYCSGTYPLMQKLRQYLYDHALNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AQFSELVNDFYNNGLPSNLTASRNPSLDYGFKGAEIAMASYCSELQYLANPVTTHVQSAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AQFSELVNDFYNNGLPSNLSGGRNPSLDYGFKGGE! AMASYCSELQFLANPVTNHVQSAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EVIRSSTKMIEREINSVNDNPLIDVSRNKALHGGNFQGTPIGVSMDNTRLAIAAIGKLMF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Summit;
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PAL2_TOBAC STANDARD; PRT; 79.35513; 022114; 01-JUN-1994 (Rel. 29, Created) 15-JUL-1998 (Rel. 36, Last sequence up 15-JUN-2002 (Rel. 41, Last annotation

update)

712 AA

Phenylalanine ammonia-lyase (EC 4.3.1.5).

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PAL2_TOBAC

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Best Local
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SITE 203 205 MODIFIED TO FORM 4-METHYLIDENE-IMIDAZOLE-
5-ONE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00221; PAL; 1.
TIGRFAMS; TIGR01226; phe_am_lyase; 1.
PROS(TE; PS00488; PAL_HISTIDASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF036948; AAC78457.1; -. HSSP; P21310; 188F.
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665 VREELGAEYLTGEKVRSPGEECDKVFTAICEGKIIDPILDCLEGWNGAPLPIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         125 QGAALQKELIRFLNAGVFGSTKESGHTLPHQATKAAMLVKINTLLQGYSGIRFEILEVIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67 SQVAAI-ATHDSG-VKVELSESARAGVKASSDWVMDSMSKGTDSYGVTTGFGATSHPPTK 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8 QNG-HKNGSVELPELCIKKOPLNWGVAAFTLKGSHLDEVKRMVAEYRKDVVKLGGESLTI 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 ENGNHVNGVVN--ELCI-KDPLNWGVAAEALTGSHLDEVKKMVAEFRKPVVKLGGETLTV 58
                                         VREELGRGFLTGEKVTSPGEEFDRVFTAMCKGQIIDPLLECLGGWNGEPLPIC
                                                                                     NGENEKNASTSIFQKIVAFEEELKVLLPKEVDSARAALDSGSAGVPNRITECRSYPLYKF
                                                                                                                                                                                                                                                                                                                                                                      FAQFSELVNDFYNNGLPSNLSGGRNPSLDYGFKGAEIAMASYCSELQFLANPVTNHVQSA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SQVAGIAAANDSDTVKVELSEAARAGVKASSDWVMESMNKGTDSYGVTTGFGATSHRRTK 118
                                                                                                                                   NGETEKNINISIFQKIATEEEELKVLLPKEVEGVRIAYENDILSIPNRIKACRSYP1.YRF
                                                                                                                                                                                  AKRTLTTGVNGELHPSRFCEKDLLKVVDREYVFAYIDDPCSATYPLMQKLRQVLVEHALT
                                                                                                                                                                                                                                AKKVLTMGVNGELHPSRFCEKDLLRVVDREYVFAYIDDVCSGTYPLMQKLRQVLVDHALN 598
                                                                                                                                                                                                                                                                                                                        EQHNQDVNSLGLLSARKTAEAVDILKLMSSTYLVALCQSIDLRHLEENMKSTVKNTVSQV 538
                                                                                                                                                                                                                                                                                                                                                                                                                    FAQFSELVNDFYNNGLFSNLSGGKNPSLDYGFKGGETAMASYCSELQFLANPVTNHVQSA 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IEVIRYSTKSIEREIDSVNDNPLIDVSRNKALHGGNFQGTPIGVSMDNTRLAIASIGKI,M
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                                                                                                                                                                                                                                                                              EQHNQDVNSLGLISSRKTAEAVDILKLMSSTFLVALCQAIDLRHLEENLRNTVKNTVSQV
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                                                                                                                                                                                                                                                                                                                                      Matches 603;
                                                                                                                                                                                                                                                                                                                                                                                                                   Lyase; Phenylpropanoid metabolism; Multigene family.

SITE 198 200 MODIFIED TO FURM 4 METHYLIDENE-IMIDAZOLE-
SOUNE (BY SIMILARITY)
SEQUENCE 712 AA: 77345 MW; E65F8A867FEA2C41 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TIGRFAMS; TIGR01226; phc_am_lyase, 1. PROSITE; PS00488; PAL_HISTIDASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long as its content modified and this statement is not removed. Usage by a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hayashida N., Okazaki M.;
Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Cloning and sequencing of a full length cDNA coding for phenylalanine ammonia-lyase from tobacco cell culture."; Plant Physiol. 104·1091-1092(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nicotiana tabarum (rommon tobarco)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta, Magnoliophyta, eudicotyledons; core eudicots;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (See http.//www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the European Bioinformatics Institute. There are no restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Taguchi G , Sharan M ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nagai
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nagai N., Kitauchi H., Shimosaka M., Okazaki M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=94218401; PubMed-8165251,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00221; PAL; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -1- FUNCTION: THIS IS A KEY ENZYME OF PLANT METABOLISM CATALYZING THE FIRST REACTION IN THE BIOSYNTHESIS FROM L-PHENYLALANINE OF A WIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001106; Phe/His_NH31yasc
193 RGTITASGDLVPLSYTAGLLTGPPNSKAVGPNGETLNAEEAFRVAGVNGGFFELQPKEGL
                                           192
                                                                                       133
                                                                                                                                                                                                                                                 13 DFCMKVDPLNWEMAADSLKGSHLDEVKKMVAEFRKPVVKLGGETLTVAQVAAIAAKDNVK 72
                                                                                                                                                                                                                                                                                        13 ELCIK-DPLNWGVAAEALTGSHLDEVKKMYAEERKPVVKLGGETLTVSQVAGIAAANDSD 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VARIETY OF NATURAL PRODUCTS HASED ON THE PHENYLPROPANE SKELETON CAPTALYTIC ACTIVITY: L-phenylalanine = trans-cinnamate + NH(3). PATHWAY: Phenylpropanoid thosynthesis, first stop SUBCELLULAR LOCATION: Cytoplasmic (Probable).

PIM: CONTAINS AN ACTIVE SITE 4-METHYLLDENE-IMIDAZOFF-5-ONE (MIO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OF RESIDUES ALA-SER-GLY (BY SIMILARITY).
SIMILARITY: BELONGS TO THE PAL / HISTIDASE FAMILY
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                                                                                                                                                                  TVKVELSEGARAGVKASSDWVMDSMGKGTDSYGVTTGFGATSHRRTKNGGALQKELIRFL 132
                                                                                 NAGVEGNGTESCHTLPGSGTRAAMLVRINTLLJGYSGIRFEILEAITKLLNHNVTPCLPL
                                                                                                                          NAGIFGNGTETSHTLPHSATRAAMIVRINTLLQGYSGIRFEILEAITKFLNNNITPCLPL 191
                                                                                                                                                                                                         TVKVELSEAARAGVKASSDWVMESMNKGTDSYGVTTGFGATSHPPTKQGGALQKELIPFL 131
                                       RCTITASGDLVPLSYIAGILTGRPNSKAVCPTCEVLNAEKAFAAACVECCFFELQPKECL 251
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86 19;
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                                                                                                                                                                                                                                                                                                                                    35: Mismatches
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              use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb.sib.ch/announce/
                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=cv. Bonny Best; MEDLINE-92291052; PubMed-1601854;
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-JUN-2002 (Ref. 41, Last annotation update)
Phenylalanine ammonia-Tyase (EC 4 3 1.5) (PAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Truncated phenylalanine ammonia lyase expression in tomato
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send
                                                                                                                                                                         WHICH IS FORMED AUTOCATALYTICALLY BY CYCLIZATION AND DEHYDRATION OF RESIDUES ALA-SER-GLY (BY SIMILARITY).
SIMILARITY: BELONGS TO THE PAL / HISTIDASE FAMILY.
                                                                                                                                                                                                                                          FIRST REACTION IN THE BIOSYNIHESIS FROM L-PHENYLALANINE OF A WIDE WARLETY OF NATURAL PRODUCTS BASED ON THE PHENYLAROPANE SKELETON. CAPALYTIC ACTIVITY: L-phenylalanine - trans-cinnamate · NH(3). PATHWAY: Phenylpropanoid biosynthesis; first step. SUBCELLULAR LOCATION: Cytoplasmic (Probable). SUBCELLULAR LOCATION: Cytoplasmic (Probable).
                                                                                                                                                                                                                                                                                                                                                                                    Biol. Chem. 267:11824-11830(1992).
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Best Local
023924;
15-JUL-1998 (Re). 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Phenylalanine ammonia-lyase (EC 4.3.1.5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; M90692; AAA34176.1; -. HSSP; P21310; 188F.
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                                                                                                    PALY_DIGLA
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                                                                                                                                                                                                              655 LYRFVREELGRGFLTGEKVTSPGEEFDRVFTAMCKGQIIDPLLECLGGWNGEPLPIC 711
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      GKLMFAQFSELVNDFYNNGLPSNLSGGRNPSLDYGFKGGEIAMASYCSELQFLANPVTNH
                                                                                                                                                                                                                                                                          HALNNGETEKNTNTSIFQKIATFEEELKVLLPKEVEGVRIAYENDTLSIPNRIKACRSYP 654
                                                                                                                                                                                                                                                                                                                                                                                                                                      GKLMFAQFSELVNDYYNNGLPLNLTAGRNPSLDYGLKGAEIAMASYCSELQFI,ANPVTNH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LGPQIEVIRAATKMIEREINSVNDNPLIDVSRNKALHGGNFQGTPIGVSMDNTRLALASI 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LGPQIEVIRSSTKMIEREINSVNDNPLIDVSRNKALHGGNFQGTPIGVSMDNTRLAIAAI 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FTDYLTHKLKHHPGQ1EAAAIMEHILDGSSYVKAAQKLHEMDPLQKPKQDRYALRTSPQW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FTDHLTHKLKHHPGQIEAAAIMEYILDGSDYVKAAQKVHEMDFLQKPKQDRYALRTSPQW 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VAGVTSGEFELQPKEGLALVNGTAVGSGMASMVLFESNILAVMSEVLSAIFAEVMNGKPE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EAITKLINSNITPCLFLRGTITASGDLVPLSYIAGLLTGRPNSKAVGPNGEKLNAEERFR 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EAITKFLNNNITPCLPLRGTITASGDLVPLSY1AGLLTGRPNSKAVGPTGEVLNAEKAFA 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RRTKNGGALQKELIRFLNAGVFGNGTESSHTLPHSATRAAMLVRINTLLQGYSGIRFEIL 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RRTKQGGALQKELIRFLNAGIFGNGTETSHTLPHSATRAAMIVRINTLLQGYSGIRFEIL 174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LTVSQVAGIA-AANDSDTVKVELSEAARAGVKASSDWVMESMNKGTDSYGVTTGFGATSH 114
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                                                                                                                                                                                                                                            HAMKNGESEKNLNSSIFQKIVAFEDELKAVLPKEVESARAVVESGNPAIPNRITECRSYP
                                                                                                                                                                                                                                                                                                          VSQVAKKTLAMGANGELHPARFCEKELLQVVEREYLFTYADDPCSSTYPLMQKLRQVLVD
                                                                                                                                                                                                                                                                                                                                      VSQVAKKVLTMGVNGELHPSRFCEKDLLRVVDREYVFAYIDDVCSGTYPLMQKLRQVLVD 594
                                                                                                                                                                                                                                                                                                                                                                       VQSAEQHNQDVNSLGLISARKTAEAVDILKLMSSTYLVALCQAIDLRHLEENLKNAVKNT 544
                                                                                                                                                                                                                                                                                                                                                                                                     VQSAEQHNQDVNSLGLISARKTAEAVDILKLMSSTYLVALCQSIDLRHLEENMKSTVKNT 534
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                                                                                                    STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    85.0%; Score 3097.5; DB 1; Length 83.4%; Pred. No. 8.3e-185;
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5-ONE (BY SIMILARITY).
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the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.ish-sib.ch/announce or send an email to license@isb-sib.ch).
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-!- FUNCTION: THIS IS A KEY ENZYME OF PLANT METABOLISM CATALYZING THE FIRST REACTION IN THE BIOSYNTHESIS FROM L-PHENYLEA-RANINE OF A WIDE VARIETY OF NATURAL PRODUCTS BASED ON THE PHENYLEA-PANE SKELETON -!- CATALYTIC ACTIVITY: L-phenylalanine - trans-cinnamate + NH(3).
-!- PATHWAY: Phenylpropanoid biosynthesis; first step.
-!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
-!- PTM: CONTAINS AN ACTIVE SITE 4-METHYLIDENE-IMIDAZOLE-5-ONE (MIO), WHICH IS FORMED AUTOCATALYTICALLY BY CYCLIZATION AND DEHYDRATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS\text{-PROT} entry is copyright. It is produced through a collaboration between the SWISS Institute of Bioinformatics and the EMBL outstation -
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae, euasterids I, Lamiales, Veronicaceae; Digitalis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00221; PAL; 1. TICRHAMS, TICRO1226, phc_am_lyase, 1. PROSITE, PS00488; PAL_HISTIDASE, 1.
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SITE 198 200 MUDIFIED TO FURM 4-MET
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                                         418 MFAQESELVNDFYNNGLPSNLSGGRNPSLDYGFKGGEIAMASYCSELQFLANPVTNHVQS 477
                                                                                                                                    360 QIEVIRTATKMIEREINSVNDNPLIDVSRNKALHGGNFQGTPIGVSMDNSRLAIASIGKL
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SIMILARITY: BELONGS TO THE PAL / HISTIDASE FAMILY.
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                                                                                                                                                                                                                                                                                                              HLTHKLKHHPGQIEAAAIMEHILDGSSYVKAAQKMHEMDPLQKPKQDRYALRTSPQWLGP
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84.0%; Pred. No. 1
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Best Local Similarity 85.7%;

Pred. No. 3.2e-184;

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RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Manners J.M., Mintyre C.L., Nourse J.P.;
"Cloning and sequence of a cDNA encoding phenylalanine anumonia-lyase
from the tropical forage legume Stylosanthes humilis.";
plant Physiol. 108-1301-1302(1995).
-1- FUNCTION: THIS IS A KEY ENZYME OF PLANT METABOLISM CATALYZING THE
FIRST REACTION IN THE HIOSYNTHESIS FROM L-PHENYLALANINE OF A WIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Viridiplantae, Streptophyta, Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids 1; Fabales, Fabaceae; Papillonoideae; Aeschynomeneae;
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01-NOV-1995 (Rel. 32, Last Sequence update)
15-JUN-2002 (Rel 41, Last annotation update)
Phenylalanine ammonia-lyase (EC 4.3.1.5).
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-I- PATHWAY: Phenylpropanoid blosynthesis; first step.

-I- SUBCRILLHAR LOCATION: Cytoplasmic (Probable).
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                                                                        SEQUENCE
                                                                                                                                                                                                             TIGREAMS; TIGR01226, phe_am_lyase, 1. PROSITE; PS00488; PAL_HISTIDASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement (See http://www.isb-sib-ch/announce/
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                                                                                                                                                                                                                                                                                         Pfam; PF00221; PAL,
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                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; L36822; AAA99500.1; -
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                                                                                                                                                                       Lyase; Phenylpropanoid metabolism.
                                                                                                                                                                                                                                                                                                                                   InterPro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: BELONGS TO THE PAL / HISTIDASE FAMILY.
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                                                                        715 AA;
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                                                                    77953 MW;
84.78;
Score 3088;
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                                                                        ONE (BY SIMILARITY).

8D81EC3D5E4F6A2D CRC64.
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15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Pel. 37, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation updat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lithospermum erythrorhizon.

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Epermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Spermatophyta; Magnoliophyta; Edward Edw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-JUN-2002 (Rel. 41, Last annotation update)
Phenylalanine ammonia-lyase 1 (EC 4.3.1.5) (PAL-1).
Biosei, Biotechnol, Biochem, 61:1995-2003(1997)
                                           "CDNA cloning and gene expression of phenylalanine ammonia-lyase Lithospermum erythrorhizon.";
                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDITINE-98101967; PubMed-9438980;
                                                                                                                                                                       Yazaki K., Kataoka M., Honda G., Severin K., Heide
                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=34254;
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	541 KVLTMGVNGELHPSRFCEKDLLKVVDREYVFAYIDDVCSGTYPLMQKLRQVIVDHAINNG 600 :	
	481 HNQDVNSLGLISARKTAFAVDILKLMSSTYLVALCQSIDLRHLFENMKSTVKNTVSQVAK 540 	
	421 QFSELVNDFYNNGLPSNLSGGRNPSLDYGFKGGEIAMASYCSELQFLANPYTNHYQSAEQ 480 	
	361 VIRSSTKMIEREINSVNDNPLIDVSRNKALHGGNFQGTPIGVSMDNTRLAIAAIGKLMFA 420 	
	301 HKLKHHPGQIEAAAIMEYILDGSDYVKAAQKVHEMDPLQKPKQDRYALRTSPQWLGPQIE 360 	
	241 GFFELOPKEGLALVNGTAVGSGMASMVLFDANVLALLSEVLSAJFAEVMOGKPEFTDHLT 300 	
	181 LNNNITPCLPLRGTITASGDLVPLSYIAGLLTGRPNSKAVGPTGEVLNAEKAFAAAGVEG 240 	
	121 GALOKELIRELNAGIEGNGTETSHTLPHSATRAAMIVRINTLLOGVSGIREEILEAITKE 180 	
	61 VAGIAAANDSDIVKVELSEAARAGVKASSDWVMESMNKGTDSYGVTTGFGATSHRRIKUG 120 	
	1 MENGNHVNGVVNELCIKDPLNWGVAAEALTGSHLDEVKKMVAEFRKPVVKLGGETLTVSO 60 	
2;	uery Match 84.5%; Score 3077.5; DB 1; Length 710; est Local Similarity 83.5%; Pred. No. 1.4e-183; atches 594; Conservative 53; Mismatches 59; Indels 5; Gaps	a a
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ition on - its way cial	gh a collaborate EMBL outstation strictions on the tin no and for commercate sib-sib.ch/announ	
	FUNCTION: THIS IS A KEY ENCYME OF PLANT METRAGLISM CAPI- FURST REAGTION IN THE BIOSYNTHESIS FROM L-PHENYLARIAN IN VARIETY OF NATURAL PRODUCTS BASED ON THE PHENYLPPOPANE CATALIZIC ACTIVITY: L-phenylalanine = trans-chonamate PATHWAY: Phenylpropanoid biosynthesis: first step. SUBCHLULLAR IOCATION: Cytoplasmic (Probable). TISSUE SPECIFICITY: EXPRESSED MAINLY IN ROOTS. THE CONTAINS AN ACTIVE SITE 4 METHYLDENE: MIDAZOLE: SHILL IS CONTAINS AN ACTIVE SITE 4 METHYLDENE: MIDAZOLE: SHILL IS CONTAINS AN ACTIVE SITE 4 METHYLDENE: MIDAZOLE: SIMILARITY: BELONGS TO THE PAL / HISTIDASE FAMILY. SIMILARITY: BELONGS TO THE PAL / HISTIDASE FAMILY.	

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Search completed: March 29, 2003, 02:10:56 Job time : 42 $\sec s$

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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
                                          Matches 617;
                                                                                                                                                                                                                                                                                                                                                                                                                     Catharanthus roseus (Rosy periwinkle) (Madagascar periwinkle). Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Gentianales; Apocynaceae; Rauvolfioldeae; Asteridae; euasterids I; Gentianales; Apocynaceae; Rauvolfioldeae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                O9MAX1;

01-0CT-2000 (TrEMBLrel. 15, Created)

01-0CT-2000 (TrEMBLrel. 15, Last sequence update)

01-JUN-2002 (TrEMBLrel. 11, Last annotation update)
                                                                                                                                                                                                                                                               "CDNA of phenylalanine ammmonia lyase from Catharanthus roseus."; Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AB042520; BAA95629.1; ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9MAX1
                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                              HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                     Vinceae; Catharanthus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Phenylalanine ammonia lyase
                                                                                                                                                              PROSITE;
                                                                                                                                                                                                                                                                                                                           Kiyota S.,
                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=4058;
                                                                                                                                                                                   TIGRFAMS,
                                                                                                                                                                                                                           InterPro;
                                                                                                                                             yase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               661
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 LNNNITPCLPLRGTITASGDLVPLSYIAGLLTGRPNSKAVGPTGEVLNAFKAFAAAGVEG
                                                             Local Similarity
2 ENGNHVNGVVNELCIKDPLNWGVAAEALTGSHLDEVKKMVAEFRKPVVKLGGETLTVSQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EHLGRGFLTGEKVTSPGEEFDRVFTAMCKGQIIDPLLECLGGWNGEPLPIC 711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HKLKHHPGQIEAAAIMEYILDGSDYVKAAQKVHEMDPLQKPKQDRYALRTSPQWLGPQIE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KVLTMGVNGELHPSRFCEKDLLRVVDREYVFAYIDDVCSGTYPLMQKLRQVLVDHALNNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HNQDVNSLGLISARKTAFAVDII.KLMSSTYLVALCQSIDI.RHI.EENMKSTYKNTVSQVAK 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           \tt VIRSSTKMIEREINSVNDNPLIDVSRNKALHGGNEQGTPIGVSMDNTRLAIAAIGKLMFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VIRSSTKMIEREINSVNDNPLIDVSRNKALHGGNFQGTPIGVSMLNTRLAIAAIGKLMFA 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       {\tt ETEKNTNTSIFQKIATFEEELKVLLPKEVEGVRIAYENDTLSIPNRIKACRSYPLYRFVR}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ETEKNTNTSIFQKIATFEEELKVLLPKEVEGVRIAYENDTLSIPNRIKACRSYPLYRFVR 660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KYLTMGVNGELHPSRFCEKDLLRVVDREYVFAYIDDVCSGTYPLMQKLRQVLVDHALNNG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QFSELVNDFYNNGLPSNLSGGRNPSLDYGFKGGEIAMASYCSELQFLANPVTNHVQSAEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QFSELVNDFYNNGLPSNLSGGRNPSLDYGFKGGELAMASYCSELQFLANPYTNHVQSAEQ 480
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                                                                                                                                                                                                                                            P21310;
                                                                                                                                                                                                    PF00221; PAL; 1
                                                                                                                                                            PS00488; PAL_HISTIDASE; 1
                                                                                                                                                                                 TIGR01226; phe_am_lyase, 1.
                                                                                                                                                                                                                         IPR001106; Phe/His_NH3lyase
                                                                                                                                                                                                                                                                                                                           Sakano K., Kim J.;
                                                                                                                        716 AA;
                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                              188F
                                                                                                                        78241 MW; 1F16D4DEB8683B0B CRC64;
                                                    87.7%; Score 3195 5; DR 10; Length 716; 86.9%; Pred No. 2.8e-194;
                                        43; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           716 AA
                                        49; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tracheophyta;
                                      1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               480
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                                                               expression, and evolution.";
Plant Physiol. 12:230-239(2001).
EMBL, AF237955, AAF40224-1, -
HSSP; P21310; 188E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae, Streptophyta; Embryophyta; Tracheog
Spermatophyta; Magnoliophyta; eudicotyledons, core eudicots,
eurosids 1, Rosales; Rosaceae; Rosoideae, Rubus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 21, Last annotation update)
Phenylalanine ammonia-lyase 2 (EC 4.3.1.5).
Pfam; PF00221; PAL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rubus idaeus (Raspberry).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9M567;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    <u>0</u>9M567
                                                                                                                                                                                                                                                                                Kumar A., Ellis B.E.
                                                                                                                                                                                                                                                                                                                           MEDLINE=21437948; PubMed=11553751;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID-32247;
                                      InterPro;
                                                                                                                                                                                                                             "The phenylalanine ammonia-lyase gene family in raspberry. structure
                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               667 DVGAEFLTGEKDRSPGEEFDKVFTAMCNEKIIDPLLECLKEWNGAPLPIC 716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                662 ELGRGFLTGEKVTSPGEEFDRVFTAMCKGQIIDPLLECLGGWNGEPLPIC 711
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               547 TLTVGVNGELHPSRFCEKDLIRVVDREYVFAYVDDPCSGTYPLMEKLRQVIVDHALQNGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       542 VLTMGVNGELHPSRFCEKDLLRVVDREYVFAYIDDVCSGTYPLMQKLRQVLVDHALNNGE 601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     302 KIKHHPGQIEAAAIMEYILDGSDYVKAAQKVHEMDPLQKPKQDRYALRTSPQWLGPQIEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      247 LFELQPKEGLALVNGTAVGSGMASMYLFEANTLAVLSEVLSATFAEVMNGKPEFTDHLTH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            127 ALQKELIRFLNAGIFGNGTESSHTLPHSATKAAMLVRINTLLQGYSGIRFEILEAITKFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              68 AAI-AARDYNAVKVELSEDARAGVKASSDWVMESMNKGTDSYGVTTGFGATSHRRTKQGG
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                                  IPR001106; Phe/His_NH31yase
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                                             PAL.1
                                                                               01-DEC-2001
01-JUN-2002
                                                          01-JUN-2002 (TrEMBLIEL. 2), Last annotation update) Phenylalanine ammonia-lyase (EC 4.3.1.5).
                                                                                                                                            Q94EN0;
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                      Rehmannia glutinosa
                                                                                                                         01-DEC-2001
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                                                                                                                                                                                                                                                               724 GEPLPIC 730
                                                                                                                                                                                                                                                                                                    705 GEPLPIC 711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        364 RYALRTSPQWLGPQIEVIRFSTKSIEREINSVNDNPLIDVSRNKALHGGNFQGTPIGVSM 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   165 GYSGIRFEILEAITKFLNNNITPCLPLRGTITASGDLVPLSYIAGLLTGRPNSKAVGPTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              124 VTTGFGATSHPPTKQGAALQKELIRFLNAGVLRNGTESAHTLPHSATRAAMLVRINTLLQ 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66 REPVEKIGGETITISQVAAI--ANHDSGVKVELAESARAGVKASSDWVMDSMNKGTDSYG 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 ENG-NHVNGVVN-----ELCIK------DPLNWGVAAEALTGSHLDEVKKMVAEF 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNTRLAIAAIGKLMFAQFSELVNDFYNNGLPSNLSGGRNPSLDYGFKGGEIAMASYCSEL 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FAEVMQGKPEFTDHLTHKLKHHPGQIEAAAIMEHILDGSSYVKAAEKLHEQDPLQKPKQD 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EVLNAEKAFAAAGVEGGFFELQPKEGLALVNGTAVGSGMASMVLFDANVLALLSEVLSAI 284
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GYSGIRFEILEAISKFLNHNITPCLPLKGTITASGDLVPLSYIAGLLTGRPNSKAVGPKG
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                                                                                                                                                                                                                                                                                                                                                                 NRIKACRSYPLYRFYREELGRGFLTGEKYTSPGEEFDRYFTAMCKGQIIDPLLECLGGWN 704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ENLKSTVKNTVSQLAKRVLTTGVNGELHPSRFCEKDLLMVVEREYLFAYIDDPCSATYPL 603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QFLANPYTNHVQSAEQHNQDVNSLGLISARKTAEAVDILKLMSSTYLVALCQSIDLRHLE 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNTRLATASIGKLMFAGFSELVNDFYNNGLPSNLSGGRDPSLDYGFKGAETAMASYCSEL 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FAEVMQGKPEFTDHLTHKLKHHPGQIEAAAIMEYILDGSDYVKAAQKVHEMDPLQKPKQD 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VTTGFGATSHRRTKQGGGALQKELIRFLNAGIFGNGTETSHTLPHSATRAAMIVRINTLLQ 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RKPVVKLGGETLTVSQVAGIAAANDSDTVKVELSEAARAGVKASSDWVMESMNKGTDSYG 104
                                                                                                                                                                                                                                                                                                                                                                                                                       MORLROVLVEHALTINGENEKNASTSTFOKTTAFEEELKTTLPKEVESARAAYESGNAALP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QFLANPVTNHVQSAEQHNQDVNSLGLISSRKTAEAVDILKLMSSTFLVALCQAIDLRHLE 543
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             MQKLRQVLVDHALNNGETEKNTNTSIFQKIATFEEELKVLLPKEVEGVRIAYENDTLSIP 644
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                                                                             (TrEMBLrel. 19, Created)
(TrEMBLrel. 19, Last sequence update)
(TrEMBLrel. 21, Last annotation updat
                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         86.4%: Score 3148.5;
83.9%: Pred. No. 2.8
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Best Local .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Molecular characterization of phenylalanine ammonia lyase Rhemannia glutinosa.";
Submitted (JUL-2001) to the EMBL/GenHank/DDBJ databases.
EMBL; AF401636; AAK64225.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TIGKEAMS: TIGKO1226; phc_am_lyase: 1.
PKOSITE: PSO0488; PAI_HISTIDASE: UNKNOWN_1.
PKOSITE: PSO0012; PHOSPHOPANTETHEINE: UNKNOWN_1
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InterPro: IPR003880; Ppantne_attach.
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Asteridae; enasterids I: Lamiales; Lamiales incertae sedis; Rehmannia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCB1_1:ax1D=99300;
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    655
                                                                                                                                     598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           236 V-SGFFELQPKEGLALVNGTAVGSGLASIALYDANILAVLSEVTSVIFAEVMNGKPEFTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      295 HUTHKLKHHPGQIRAAAIMEHILDGSAYVKAAQKUHETDPLQKPKQDRYALRTSPQWLGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                / Match 85.3%; Score 3107.5; DB 10; Longth 708; Local Similarity 84.3%; Pred. No. 1.1e-188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MENGNHVNGVVNELCI---KDPLNWGVAAEALTGSHLDEVKKMVAEFRKPVVKLGGETLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MENGHHIS---NGLOVETTROPLNWVAAAPSLKGSHIJJEVKKMVELEKKVAVKLGGESLT 57
FIREELGTNYLTGEKVVSPGEECDKVFTALSKGLIVDPLLKCLEGWNGAPPPIC 708
                                          FVREELGROFILIGEKVTSPOLEFIERVFTAMCKOQ11bPLLECLGGWNGEPLP1C 711
                                                                                                                                                                                                                     VAKKVLTMGVNGELHPSRECEKDLLRVVI REYVEAYIDDVCSGTYPLMQKLRQVLVDHAL
                                                                                                                                                                                                                                                                                                                                                                                                   MFAQFSELVNDFYNNGLPSNLSGGRNPSLDYGFKGGETAMASYCSELOFLANPVTNHVQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                  QIEVIRTATKMIEREINSVNDTPLIDVSRNKALHGGNFQGTPIGVSMDNTKLAIAAIGKI. 4]4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QIEVIPSSTKMIEREINSVNDNPLIDVSPNKALHGGNEQGIPIGVSMDNTRLAIAAIGKL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TKELNNNITPCLPLPGTITASGDLVPLSYIAGLLTGPPNSKAVGPTGEVLNAEYAFAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KQGGALQKELIRFLNAGIFGNGTESNHALPHSATRAAMLVRINTLLQGYSGIRFEILEAL 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KQGGALQKELLRELNAGTEGNGTETSHTLPHSATRAAMTVRINTLLQGYSGTREETLEAT 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VSQVAGIAAANDSDTVKVELSEAARAGVKASSDWVMESMNKGTDSYGVTTGFGATSHRRT 117
                                                                                    NNGESEKNYSTSIFOKIEAFEVELKAILPKEVESARIALESGNPAIGNRITECRSYPLYK
                                                                                                                                                                           VAKRTLIMG1NGELHPSRFCEKDLLRVVDREYVFAY1DDPCSGTYPLMQKLRQVLVDHAL
                                                                                                                                                                                                                                                                  AEQHNQDVNSLGLLSSRKTVEALDILKLMSSTYLTALCQAVDLRHLEENLRLSVKNTVSQ
                                                                                                                                                                                                                                                                                                            AEQHNQDVNSLGLISARKTAEAVDILKLMSSTYLVALCQSIDLKHLEENMKSIVKNTVSQ
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                                                                                                                                 NNGETEKNENTS LEGK LATEEEELKVILLEKEVEGVK LAYENDILLS LENKI KACKSYELYK
                                                                                                                                                                                                                                                                                                                                                         MEAQESELVNDEYNNGLESNLSGGENESLDYGEKGSEIAMASYCSELQFLANPVTNHVQS
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09XFX5;
01-NOV-1999 (TrEMBLrcl. 12, Created)
01-NOV-1999 (TrEMBLrcl. 12, Last sequence update)
01-JUN-2002 (TrEMBLrcl. 21, Last annotation update)
phenylalanine-ammonia lyase (EC 4.3 1 5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Phenylalanine ammonia-lyase gene expression in response to low temperature in mandarin iruit."; Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
EMBL: AJ238753; CAB42793.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9XFX5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sanchez-Ballesta M.T., Lafuente M.T., Zacarias L., Granell A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-CV
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544 TVSQVARKVLTVGANGELHPSRFCEKDLLKAADREHVFAYIDDPCSATYPLMQKLRQVLV 603
                                                                                                                                                                                                             414
                                                                                                                                                                                                                                                                                                                                       304
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                                        534 TVSQVAKKVLIMGVNGELHPSKECEKDLLRVVDREYVFAYIDDVCSGTYPLMQKLRQVLV 593
                                                                                                                                                                                                                                                                                                                                                                                                                                                        234 AAAGVEGGFFELQPKEGLALVNGTAVGSGMASMVLFDANVLALLSEVLSAIFAEVMQGKP 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      114 HRRTKQGGALQKELIRFLNAGIFGNGTETSHTLPHSATRAAMIVRINTLLQGYSGIRFEI 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 IENG-HONGCLEGICKDNNYSSGDALNWGVMAETIKGSHLEEVKRMVAEYRKPVVNLGGE 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MENGNHVNGVVNELC-----IKDPLNWGVAAEALTGSHLDEVKKMVAEFRKPVVKLGGE 54
                                                                                                                                                                                                                                                                      WLGPQIEVIRSSTKMIEREINSVNDNPLIDVSRNKALHGGNFQCTPIGVSMDNTRLAIAA 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TLTVSQVAGIAAANDSDT-VKVELSEAARAGVKASSDWVMESMNKGTDSYGVTTGFGATS 113
                                                                                                                         HVQSAEQHNQDVNSLGLISARKTAEAVDILKLMSSTYLVALCQSIDLRHLEENMKSTVKN 533
                                                                                                                                                                                                      IGKLMFAQFSELVNDFYNNGLPSNLSGGKNFSLDYGFKGGELAMASYCSELQFLANPVTN 473
                                                                                                                                                                                                                                                 WLGPQIEVIRFATKSIEREINSVNDNPLIDVSRNKALHGGNFQGTPIGVSMDNTRLAIAA 423
                                                                                                                                                                                                                                                                                                                                EFTDHLTHKLKHHPGQIEAAAIMEHILDGSSYVKAAKKLHEIDPLQKPKQDRYALRTSPQ
                                                                                                                                                                                                                                                                                                                                                                                                               KQAGE - - GEFELQPKEGLALVNGTAVGSGLASMYLFDANNLALLSEILSAIFAEVMQGKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LEAITKFLNNNITPCLPLRGTITASGDLVPLSYIAGLLTGRPNSKAVGPTGEVLNAEKAF 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TLTVAQVAATATAGDVNAQVKVELSESAPEGVKASSDWVMDSMNKGTDSYGVTTGFCATS
                                                                                   HVQSAEQHNQDVNSLGLISSKKTAEAVDILKLMSSTFLVALCQAIDLRHLEENLKHTVKD
                                                                                                                                                                IGKIMFAQFSELVNDFYNNGLPSNLSGGRNPSLDYGFKGAETAMASYCSELQFLANPVTN 483
                                                                                                                                                                                                                                                                                                                                                                     EFTDHLTHKLKHHPGQIEAAAIMEYILDGSDYVKAAQKVHEMDPLQKFKQDKYALRTSPQ 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LDAITKLLNHSITPCLPLRGTITASGDLVPLSYIAGLLTGRENSKATGPNGEIIDAQEAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HRRTQNGCALQKELIKFLNAGIFGNGTKSSHTLPHSATRAAMLVRVNTLLQGYSGIRFEI 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PF00221; PAL; 1.

AMs; TIGR01226; phe_am_lyase; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            85.2%; Score 3106; DB 10; 84.3%; Pred. No. 1.4e-188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48; Mismatches 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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QAXI5;
QAXI5;
QI-JUN-2001 (TrEMBLrel. 17, Created)
QI-JUN-2001 (TrEMBLrel. 17, Last sequence update)
QI-JUN-2002 (TrEMBLrel. 21, Last annotation update)
QI-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Phenylalanine ammonia-lyase (EC 4.3.1.5).
Pharbitis nil (Violet) (Japanese morning qlory).
Pharbitis nil (Violet) (Japanese morning clory).
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TIGRFAMS; TIGR01226; phe_am_lyase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Astoridae; euasterids I; Solanales; Convolvulaccae; Ipomoea.
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420 AQFSELVNUYYNNGLPSNLTAGRNPSLUYGFKGAEIAMASYCSELQFLANPVTNHVQSAE 479
                                               420 AQFSELVNDFYNNGLPSNLSGGRNPSLDYGFKGGETAMASYCSELQFLANPVTNHVQSAE 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00488; PAL_HISTIDASE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro;
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                                                                                                                                                                                      300 THKLKHHPGQIEAAAIMEHILDGSSYVKAAQKMHEMDPLQKPKQDRYALRTSPQWLGPQI 359
                                                                                                                                                                                                                                        300
                                                                                                                                                                                                                                                                                  240 GGFFELQPKEGLALVNGTAVGSGMASMVLFEANVLAVLSEVLSAIFAEVMNGKPEFTDHL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       604 EHALNNGENEKNANSSIFQKIAAFEEELKAVLPKEVENARQTVENGNPTIPNRIKECRSY 663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    594 DHALNNGETEKNTNTSIFQKIATFEEELKVLLPKEVEGVRIAYENDTLSIPNRIKACRSY 653
                                                                                            360 EVIRAATKMIEREINSVNDNPLIDVARSKALHGGNFQGTPIGVSMDNSRLALASIGKILF 419
                                                                                                                                                                                                                                                                                                                                  240 GGFFELQPKEGLALVNGTAVGSGMASMYLFDANVLALLSEVLSALFAEVMQGKPEFTDHL 299
                                                                                                                                                                                                                                                                                                                                                                                    180 LLNHNITPCLPLRGTITASGDLVPLSYIAGLITGRPNSKAVGPNGETLNAEEALRLAGVN
                                                                                                                                                                                                                                                                                                                                                                                                                            180 FLNNNITPCLPLRGTITASGDLVPLSYIAGLLTGRPNSKAVGPTGEVLNAEKAFAAAGVE 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                120 GGALQKELIRFLNAG1FGNGTESCHTLPHSATRAAMLVRINTLLQGYSGIRFEILEAITK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120 GGALQKELIRFLNAGIFGNGTETSHTLPHSATRAAMIVRINTLLQGYSGIRFEILEAITK 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 QVAAIASRDNA--VTVELSEESRAGVKASSDWVMDSMNKGTDSYGVTTGFGATSHPRTKQ 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60 QVAGIAAANDSDTVKVELSEAARAGVKASSDWVMESMNKGTDSYGVTTGFGATSHRRTKQ 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 LQNNGHQNG----FCVKVDPLNWEVAADSLRGSHLDEVKVMVAEFRKPAVKLGGETLTVA 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EVIRSSTKMIEREINSVNDNPLIDVSRNKALHGGNFQGTPIGVSMDNTRLAIAAIGKLMF 419
                                                                                                                                                                                                                                     THKLKHHPGQIEAAAIMEYILDGSDYVKAAQKVHEMDPLQKPKQDRYALKTSPQWLGPQI 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       85.1%; Score 3100.5; DB 10; Length 711; 84.3%; Pred. No. 3e-188;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Cassava phenyialanine ammonia-lyase expressed during post-harvest physiological deterioration "; Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AY036011, AAK62030.1, ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Manihot esculenta (Cassava) (Manioc).
Eukaryota, Viridiplantae, Streptophyta, Emeryophyta, Tracheophyta;
Spermalophyta: Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-DEC-2001 (TERMBLEC! 19, Created)
01-DEC-2001 (TERMBLEC! 19, Last sequence ipdate)
01-JHW-2002 (TERMBLEC! 21, Last annotation update)
Phenylalanine ammonia-lyase 1 (EC 4.3.1.5).
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TIGRFAMs; TIGR01226; phe_am_lyase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00488; PAL_HISTIDASE; UNKNOWN_1.
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317
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                                                                                                                                                    197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                              19 DPLNWGMAAESLKGSHIDEVKRMVDEYRKPVVRLGGETLTIAQVTAI -- ANHDSGVKVEL 76
                                                                                                                                                                                                                                                                                                                                                                                                                18 DPLNWGVAAEALTGSHIDEVKKMVAEERKPVVKLGGETLTVSQVAGIAAANDSDTVKVEL 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Y., Beeching J.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GETEKNTNTS (FQK LATFEEELKVILLPKEVEGVRIAYENDTLS) PNR IKACRSYPLYRFV 659
HVLDGSSYIKAAQKVHEIDPLQKPKQDRYALRTSPQWLGPQIEVIRTATKMIEREINSVN 376
                    YILDGSDYYKAAQKYHEMDPI.QKPKQDRYALRTSPQWLGPQTEVTRSSTKMTERETNSVN 377
                                                                                                                                                                                                                                                NGTETSHTLPHSATRAAMIVRINTLLQGYSGIREEILEAITKFLNNNITPCLPLRGTITA 197
                                                                                                                                                                                                                                                                                                                        SEAARAGVKASSDWVMESMNKGTF/SYGVTTGFGATSHPF/TKg/SGALGKELIRFLNAG1FG 137
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                                                                                                                                            SHEARAGVKASSDWVLDSMNKGTDSYGVTTGFGATSHRRTKQGGALQRELIRFLNAGIFG 136
                                                                      AVGSGLASMVLFEANVLAVLSEVLSALFAEVMLGKPEFTDHLTHKLKHHPGQTEAAATME
                                                                                                            AVGSGMASMVLEDANVLALLSEVLSAIFAEVMOGKPEFTDHLTHKLKHHPGOIEAAAIME 317
                                                                                                                                                                                    SGDLVPLSY LAGLLTGRPNSKAVGPTGEVLNAEKAFAAAGVEGGFFELQPKEGLALVNGT 257
                                                                                                                                                                                                                          NGQESCHTLSHTATRAAMLVRINTLLQGYSGIRFEILEAITKFINNNVTPRLPLRGTITA 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                              592;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      710 AA; 77559 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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85.3%; Pred. No. 9
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RESULT 8
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09AIN?
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TIGREAMS; TIGRO1226; phc_am_lyase; 1. PROSITE; PS00488; PAL_HISTIDASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota: Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta; Magnoliophyta; endicotyledous; core endicots;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         *Molecular Cloning and Characterization of Phenylalanine Ammonia-
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177 ITKELNNNITPCLFLEGTITASGDLVFLSYIAGLLIGEPNSKAVGFIGEVLNAEKAFAAA
                                                                                                                                                                                                                                        64 TISQVAATAAKDNA--VAVELAESAFAGVKASSDWVMDSMSKGTDSYGVITGIGATSHER 121
                                                                                                                                                                                                                                                                                                                                                                                              4 NGHHOSNGHNUGANGFOVKONDULNWAAAAFSI.KGSHI.FFVKKWVFFFFVKPVKI.GGETI. 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 NGNH----VNGVVNELFIK--DPLNWGVAAEALTGSHLDEVKKMVAEFPKPVVKLGGETL 56
                                                                                                                    TKOGGALQKELLRELMAGIFGNGTETSHTLPHSATRAAMIVRINTLLQGYSGIRFEILEA 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LTGGRNPSLDYGFKGAEIAMASYCSELQFLANFVTNHVQSAEQHNQDVNSLGLISSRKTA 496
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                                                                                                                                                                                                                                                                                                                   TVSQVAGIAAANDSDTVKVELSHAARAGVKASSDWVMESMNKGTDSYGVTTGFGAISHRR 116
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RESULT 9
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                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trachcophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Malpighiales; Euphorbiaceae; Manihot.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-DEC 2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Phenylalanine ammonia-lyase 2 (EC 4.3.1.5).
                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00221; PAL; 1.
TIGRFAMS; TIGR01226; phe_am_lyase,
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases EMBL; AF383152; AAK60275.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q94F89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q94F89
                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00488; PAL_HISTIDASE; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=3983;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Manihot esculenta (Cassava) (Manioc)
                                                                                                                                                                                                                                                                                                                                Lydse
                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Phenylalanine ammonia-lyase 2 gene, PAL2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Li H., Beeching J.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                182 ITKELNQNVTPYLPLPGTITASGDLVPLSYIAGLLTGRPNSKAVGPAGEPLTAEQAFKLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              242 GVTGGFFDLQPKEGLALVNGTAVGSGLASIALFDANVLAVLSVVMSPVFAEVMNGKPEFT
                              61
                                                                                                                                                                                                                     Local Similarity
                                                                                    6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REVREELGRGELTGEKYTSPGEEFDRYFTAMCKGQIIDPLLECLGGWNGEPLPIC 711
                            VAGIAAANDSDTVKVELSEAAPAGVKASSDWVMESMNKGTDSYGVTTGFGATSHPPTKQG 120
                                                                              QNG-HQNGSLDSLCTARDPLNWGLAAESMSGSHLDEVKKMVAEFRKPLVKLGGETLTVAQ 64
                                                                                                                                 ENGNHVNGVVNELC-IKDPLNWGVAAEALTGSHLDEVKKMVAEERKPVVKLGGETLTVSQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KFIREELGTGFLTGEKAVSPGEECEKVFAALSNGLIIDPLLECLQCWNGEPLPIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LLFAQFSELVNDFYNNGLPSNLSGGRNPSLDYGFKGSEIAMASYCSELQFLVNPVTNHVQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QVAKRTLTMGVNGELHPSRFCEKELIRVVDREYVFTYIDDPCLATYPLMQKLRQVLVDHA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SAEQHNQDVNSLGLISARKTAEAVDILKLMSSTYLVALCQSIDLRHLEENMKSTVKNTVS 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LMFAQFSELVNDFYNNGLPSNLSGGRNPSLDYGFKGGETAMASYCSELQFLANPVTNHVQ 476
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                                                                                                                                                                                            593;
                                                                                                                                                                                                                                                                                                                                                                                                                                   IPR001106; Phe/His_NH3lyase
                                                                                                                                                                                                                                                                                                       712 AA;
                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
77462 MW;
                                                                                                                                                                                                                   84.6%; Score 3084.5; DB 1083.4%; Pred. No. 3.1e-187;
                                                                                                                                                                                         62; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                    99F14CB9D0DEA34D CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  from cassava.";
                                                                                                                                                                                                                                            DB 10, Length 712,
                                                                                                                                                                                            Indels
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                            A CONTRACTOR OF THE CONTRACTOR
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RESULT 10
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                                                                                                                                                                                                        "Phenylalanine ammonia-lyase gene expression in response to temperature in mandarin fruit."; submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases. EMBL; AJ238754; CAB42794.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Citrus clementina x Citrus reticulata.
Eukaryota; Viridiplantae, Streptophyta; Embryophyta, Tracheophyta;
Spermatophyta, Magnoliophyta, eudicotyledons; core eudicots; Rosidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
SEQUENCE
                                                     PROSITE; PS00488; PAL_HISTIDASE;
                                                                              Pfam; PF00221; PAL; 1.
TIGRFAMS; TIGR01226; phe_am_lyase; 1.
                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                             eurosids II; Sapindales; Rutaceae; Citrus.
NCBI_TaxID=93374;
                            Lyase
                                                                                                                                                                                                                                                                                                                         Sanchez-Ballesta M.T., Lafuente M.T., Zacarias L., Granell A.
                                                                                                                                                                                                                                                                                                                                                           STRAIN-CV. FORTUNE; TISSUE-FLAVEDO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Phenylalanine-ammonia lyase (EC 4.3.1.5).
                                                                                                                                                                               HSSP; P21310; 1B8F
                                                                                                                                                   [nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            662 EEIGTGLLTGEKIRSPGEEFDKVFTAMCQGKILDPMLDCLKEWNGAPLPIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         541 KVLTMGVNGELHPSRFCEKDLLRVVDREYVFAYIDDVCSGTYPLMQKLRQVLVDHALNNG
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            Osakabe Y., Ohisubo Y., Kawai S., Katayama Y., Moroboshi N.; "Structures and tissue-specific expression of genes for phenylalanine ammonia-lyase from a hybrid aspen, Populus kitakamiensis."; Plant Sci, 105:217-225(1995).
                                                                                                                                                     Eukaryota: Viridiplantae, Streptophyta, Embryophyta, Trachec
Spermatophyta: Magnoliophyta: endicotyledons: core endicots,
eurosids I: Majpighiales: Salicaceae: Populus.
                                                                                                                                                                                                                                    01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Phenylalanine ammonia-lyase (EC 4.3.1.5).
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                                                                                                                                                                                                                 Populus kitakamiensis (Aspen).
                                                                                                                                      NCBI_TaxID-3698;
                                                                                                  SEQUENCE FROM N.A.
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D30656; HAA21643.1;
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Q94AN1 PPELIMINARY: PRT: 725 AA.
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TIGPFAMs: TIGP01226: phe_am_lyase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Full Length chNA of gene TIJB.22/At2g37040 (G::6598547)."; Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AY045919; AAK76593.1; -.
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PRINTS; PR01568; LYMPHOTACTNP
TIGRFAMS: TIGR01226; phc_am_lyaso; 1.
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                                                 648 KACRSYPLYREVREELGRGFLTGEKVTSPGEEFDRVFTAMCKGQIIDPLLECLGGWNGEP 707
                                                                                                                                                                                                  542 RQTVKNTVSQVAKKVLTTGVNGELHPSRFCEKDLLKVVDREQVYTYADDPCSATYPLIQK 601
                                                                                                                                                                                                                                                                                                                                                468 ANPVINHVQSAEQHNQDVNSLGLISARKTAEAVDILKLMSSTYLVALCQSIDLRHLEENM
                                                                                                                                                                                                                                                                                                                                                                                                    422 RLAIAAIGKLMFAQFSELVNDFYNNGLPSNLTASRNPSLDYGFKGAEIAMASYCSELQYL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     348 LRTSPQWLGPQIEVIRSSTKMIEKEINSVNDNPLIDVSRNKALHGGNFQGTPIGVSMDNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   242 TAEEAFKLAGISSGFFDLOPKEGLALVNGTAVGSGMASMVLFETNVLSVLAEILSAVFAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               228 NAEKAFAAAGVEGGFFELQPKEGLALVNGTAVGSGMASMVLFDANVLALLSEVLSAIFAE 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             168 GIRFEILEAITKFLNNNITPCLPLRGTITASGDLVPLSYIAGLLTGRPNSKAVGPTGEVL 227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   182 GIRFEILEAITSFLNNNITPSLPLRGTITASGDLVPLSYIAGLLTGRPNSKATGPNGEAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 NGNHVN---GVVNELC------IKDPLNWGVAAEALTGSHLDEVKKMVAEFRKP 47
KECRSYPLYRFYREELGTELLTGHKYTSPGEEFDKYFTAICEGKILDPMMECLNEWNGAP
                                                                                                                                                                                                                                                                                                 ANPVTSHVQSAEQHNQDVNSLGLISSRKTSEAVDILKLMSTTFLVAICQAVDLRHLEENL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VMSGKPEFTDHLTHRLKHHPGQ1EAAAIMEHILDGSSYMKLAQKLHEMDPLQKPKQDRYA 361
                                                                                                                                                   LROVLVDHALNNGETEKNTNTSTFOKTATFEEELKVLLPKEVEGVRTAYENDTLSTPNRT
                                                                                                                                                                                                                                                KSTVKNTVSQVAKKVLTMGVNGELHPSRFCEKDLLRVVDREYVFAYIDDVCSGTYPLMQK 587
                                                                                                  LRQVIVDHALINGESEKNAVTSIFHKIGAFEEELKAVLPKEVEAARAAYDNGTSAIPNRI
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81.4%; Pred. No. 9.6
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Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_Tax1D=3702;
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484 DVNSLGLISARKTAEAVDILKLMSSTYLVALCQSIDLRHLEENMKSTVKNTVSQVAKKVL 543
                                                                                                                                                                                                                                                            424 ELVNDFYNNGLPSNLSGGRNPSLDYGFKGGEIAMASYCSELQFLANPVTNHVQSAEQHNQ 483
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                                                                                                                                                                                                                                                                                                                                                                                                                                        364 SSTKMIFREINSVNDNPLIDVSRNKALHGGNFQGTPIGVSMDNTRLAIAAIGKLMFAQFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   304 KHHPGQIEAAAIMEYILDGSDYVKAAQKVHEMDPLQKPKQDRYALRTSPQWLGPQIEVIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              250 DLQPKEGLALVNGTAVGSGMASMVLFEANVQAVLAEVLSAIFAEVMSGKPEFTDHLTHRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          244 ELQPKEGLALVNGTAVGSGMASMYLFDANVLALLSEVLSAIFAEVMQGKPEFTDHLTHKL 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     190 NISPSLPLRGTITASGDLVPLSYIAGLLTGRPNSKATGPDGESLTAKEAFEKAGISTGFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             184 NITPCLPLRGTITASGDLVPLSYTAGLLTGRPNSKAVGPTGEVLNAEKAFAAAGVEGGFF 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       130 QTELIRFLNAGIFGNTKETCHTLPQSATRAAMLVRVNTLLQGYSGIRFEILEAITSLLNH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        124 QKELIFFLNAGIFGNGTETSHTLPHSATRAAMIVPINTLLQGYSGIPFEILEAITKFLNN 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12 GEKTKVAVTTKTLADPLNWGLAADQMKGSHLDEVKKMVAEYRRPVVNLGGETLTIGQVAA 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 GNHVNGVVNELCIKDPLNWGVAAEALTGSHLDEVKKMVAEFRKPVVKLGGETLTVSQVAG 63
                                                                                                                                                                                ELVNDFYNNGLESNLTASSNESLDYGEKGAELAMASYCSELQYLANEVTSHVQSAEQHNQ
                                                                                                                                                                                                                                                                                                                                                           QATKSTEREINSVNUNPLIUVSRNKAIHGGNFQGTFIGVSMUNTRLALAAIGKLMFAQFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KHHPGQ1EAAA1MEH1LDGSSYMKLAQKVHEMDPLQKPKQDRYALRTSPQWLGPQ1EV1R
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81.6%; Pred. No. 20
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RESULT 14
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-DEC-2001 (TrEMBLEE: 19, Created)
01-DEC-2001 (TrEMBLEE: 19, Last sequence update)
01-JUN-2002 (TrEMBLEE: 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Phenylalanine ammonia-lyase 1 gene, PALI, from cassava.";
Submitted (MAY-2001) to the EMBL/GenHank/DDHJ databases.
EMRL: AF383151; AAK60274.1,
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Pfam; PF00221; PAL; 1.
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                                                                                317
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18 DPLNWGVAAEALTGSHLDEVKKMVAEFRKPVVKLGGETITVSQVAGTAAANDSDTVKVEL 77
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UNPLIDVSKNIALHGGNEGGTPIGVSMDNIKLAIASIGKLMEAGESELVNDEYNNGLPSN 436
                                                                                                                 YILDGSDYVKAAQKVHEMDPLQKPKQDRYALRTSPQWLGPQIEVIRSSTKMIEREINSVN 377
                                                                                                                                                                                                                                                                             SGDLVPLSYTAGLLTGRPNSKAVGPTGEVLNABKAFAAAGVEGGFFELQPKEGLALVNGT 257
                                                                                                                                                                                                                                                                                                                                       NGTETSHTLPHSATRAAMIVRINTLLQGYSGIRFEILEAITKFLNNNITPGLPLRGTITA 197
                                                                                                                                                                                                                                                                                                                                                                                               SEEARAGVKASSDWVLDSMNKGTDSYGVTTGFGATSHFFTK@GGALQRELIRFLNAGIFG
                                       DNPLIDVSRNKALHGGNEQGTPIGVSMDNTRLAIAAIGKLMFAQFSELVNDFYNNGLPSN 437
                                                                            HVLDGSSYIKAAQKVHEIDPLQKPKQDRYALRTSPQWLGPQIEVIRTATKMIEREINSVN
                                                                                                                                                           AVGSGLASMVLFEANVLAVLSEVLSATFAEVMLGKPEFTDHLTHKLKHHPGQTEAAAIME
                                                                                                                                                                                                AVGSGMASMVLEDANVLALLSEVLSATFAEVMQGKPEFTDHLTHKLKHHPGQTEAAAIME 317
                                                                                                                                                                                                                                       SCOLVELSYTAGLI TGPPNSKSLGPNGESLDAAEAFKLAGINGGFFELQPKEGLALVNGT 256
                                                                                                                                                                                                                                                                                                                    NGQESCHTLSHTATRAAMLVKINTLLQGYSGIRFEILEAITKFINNNVTPRLPLRCTITA 196
                                                                                                                                                                                                                                                                                                                                                                                                                                    SHAARAGVKASSDWVMESMNKGTDSYGVTTGEGATSHRRTKQGGALQKELLRELNAGIEG 137
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75065 MW; 950A63A1A4BE3D76 (PC64;
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85.8%; Pred No. 1 4e-181;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Isolation of phenylalanine ammonia:lyase gene from Vigna unguiculata, challenged by cucumber mosaic virus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ų9XGR3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (JÜL-1999) to the EMBL/GenBank/DDBJ databases EMBL; AF165998; AAD45384.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Spermatophyta, Magnoliophyta, eudicotyledons; core eudicots; kosidae; eurosids I, Fahales, Fahaceae, Fapilionoideae, Fhaseoleae, Vigna.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vigna unguiculata (Cowpea).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Phenylalanine ammonia-lyase (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ffam, FF00221, PAL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP, P21310; 1B8F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kang K.J., Kim S.H., Park Y.I.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                      176 AITKFLNNNITPCLPLRGTITASGDLVPLSYIAGLLTGRPNSKAVGPTGEVLNAEKAFAA 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        116 KIKQGGALQKELIFFLNAGIFGNGTETSHTLPHSATFAAMIVFINTLLQGYSGIRFEILE 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        56 LIVSQVAGIAAANDSDIVKVELSEAAKAGVKASSDWVMESMNKGIDSYGVITGFGATSHR 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 LTVSQVAAVATCHDR-RVTVELAGESRPGVKASSDWVIDSMSRGTDSYGVTTGFGATSHR 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EKDLLKVVDREYVYAYVDDPCSATYPLMQKLRQVLVDHAMMNGEKEKNSSTSIFQK1GAF 616
                                  TDHLTHKLKHHPGQIEAAAIMEYILDGSDYVKAAQKVHEMDPLQKPKQDRYALRTSPQWL
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TDHLTHKLKHHPG0TEAAATMEHTLDGSSYTKEAQKLHETDPLQKPKQDRYALKTSPQWL
                                                                                                                                          AEIDGGFFELQPKEGLALVNGTAVGSGLASIVLFEANLLVVLTEVLSAIFAEVMQGKPEF
                                                                                                                                                                                                               AGVEGGEFELQPKEGLALVNGTAVGSGMASMVLFDANVLALLSEVLSATFAEVMOGKFEF 295
                                                                                                                                                                                                                                                                                    AITKFLNHNITPCLPLRGTITASGDLVPLSYVAGLLIGRPNSKSIGPNGEDLNAKDAFKL
                                                                                                                                                                                                                                                                                                                                                                                                                                   RTKQGGALQNELI RELNAG I EGNGTEASHTLPYSSTRAAMLVRVNTILLQGYSG I REDIME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       538;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TIGR01226; phe_am_lyase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  655 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          71874 MW; 1F1DC76B49A538BF CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              77.4%; Score 2820.5; 82.0%; Pred. No. 1.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
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	YKFYRESLGTSLQYGEKYKSPGEECDKVFTALCEGKFIDPMMDCLKKWNGSPLPIC 655	600	Дb
	<	656	Qy
599	ALQNGEKEASSSTSIFHKIRAFEEELITLLPKEVENARVEVENGNSSIPNRIKECRSYPL	540	DЪ
655	ALNNGETEKNTNTSIFQKIATFEEELKVLLPKEVEGVRIAYENDTLSIFNRIKACRSYPL	596	Ϋ́
539	SQVAKRVLTTGINGELHPSRFCEKDLLKIVDHEYVFAYIDDPCSVTYPI,MQKLRSVLVDH	480	DЪ
595	SQVAKKVLTMGVNGELHPSRFCEKDLLRVVDREYVFAYIDDVCSGTYPLMQKLRQVLVDH	536	Qy
479	0-	420	рь
53.5	QSAEQHNQDVNSLGLISARKTAEAVDILKLMSSTYLVALCQSIDLRHLEENMKSTVKNTV	476	QУ
419	KLMFAQFSELVNDFYNNGLPSNLTAGRNPSLDYGFKGAEIAMASYCSELQYLANPVTNHV	360	DЪ
475	KLMFAQFSELVNDFYNNGLPSNLSGGRNPSLDYGFKGGEIAMASYCSELQFLANPVINHV	416	Ϋ́
359	GPQ1EVIRHATKM1EREINSVNUNPL1DVSRNKALHGGNFQGTP1GVSMDNTRLAIASIG	300	Dр
415	GFQIEVIRSSTKMIEKEINSVNDNPLIDVSRNKALHGGNFQGTPIGVSMDNTRLAIAAIG	356	Š

Search completed: March 29, 2003, 02:12:14 Job time : 67 secs